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(21) International Application Number: PCT/US96/01585 (22) International Filing Date: 1 February 1996 (01.02.96) (30) Priority Data: 08/383,756 2 February 1995 (02.02.95) US 08/460,898 5 June 1995 (05.06.95) US (60) Parent Application or Grant (63) Related by Continuation US Not furnished (CIP) Filed on Not furnished (71) Applicant (for all designated States except US): CALGENE, INC. [US/US]; 1920 Fifth Street, Davis, CA 95616 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): DEHESH, Katayoon [US/US]; 521 Crownpointe Circle, Vacaville, CA 95687 (US). VOELKER, Toni, Alois [DE/US]; 1206 Cowell Place, Davis, CA 95616 (US). HAWKINS, Deborah [US/US]; 230 Grande Avenue, Davis, CA 95616 (US). (74) Agents: SCHWEDLER, Carl, J. et al.; Calgene, Inc., 1920 Fifth Street, Davis, CA 95616 (US).	(81) Designated States: CA, JP, US, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 5 December 1996 (05.12.96)	
(54) Title: PRODUCTION OF MYRISTATE IN PLANT CELLS (57) Abstract <p>By this invention, methods to produce C14 fatty acids in plant seed oils are provided. In a first embodiment, this invention relates to particular C14 preferring acyl-ACP thioesterase sequences from <i>Cuphea palustris</i>, camphor and nutmeg, and to DNA constructs for the expression of these thioesterases in host cells for production of C14 fatty acids. Other aspects of this invention relate to methods for using other plant medium-chain thioesterases or medium-chain thioesterases from non-plant sources to provide C14 fatty acids in plant cells. In this regard, the production of C14 fatty acids in plant cells as the result of expression from <i>Cuphea palustris</i>, nutmeg and camphor medium chain acyl-ACP thioesterases is provided.</p>		

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PRODUCTION OF MYRISTATE IN PLANT CELLS

5 This application is a continuation-in-part of USSN
08/383,756 filed February 2, 1995.

Technical Field

10 The present invention is directed to nucleic acid
sequences and constructs, and methods related thereto.

INTRODUCTION

Background

15 Members of several plant families synthesize large amounts
of predominantly medium-chain (C8-C14) triglycerides in
specialized storage tissues, some of which are harvested for
production of important dietary or industrial medium-chain
fatty acids containing oils (F.D. Gunstone, *The Lipid Handbook*
(Chapman & Hall, New York, 1986) pp. 55-112). Lauric oil
20 (those containing C12:0 fatty acyl groups) and its derivatives
find widespread use, particularly in the soap, detergent and
personal care industries.

Over the past several years, mildness has become
increasingly important in differentiating soaps, detergents
25 and personal care products, with an emphasis on developing
surfactants that combine acceptable performance with improved
mildness. Myristate (C14:0) based surfactants offer an
excellent combination of cleansing and mildness. However,
limitations on the supply of myristate have precluded
30 significant use of these surfactants, despite their functional
superiority in certain applications. Myristate is available
only in relatively small quantities as a coproduct of the
fractionation of lauric oils. Coconut oil contains
approximately 48% C12:0 and 17% C14:0, and palm kernel oil
35 contains approximately 51% C12:0 and 18% C14:0. Only a
fraction of the C14:0 present in these oils, however, is
available as purified C14:0 (myristate), as most commercial
"lauric fatty acid/methyl ester" products contain significant
amounts of myristate, in addition to the primary laurate

component. Thus, myristate based derivatives currently find only limited use in the personal care product industry due to the high cost involved in their production.

5 Literature

- Pollard, et al., (Arch. of Biochem. and Biophys. (1991) 284:1-7) identified a medium-chain acyl-ACP thioesterase activity in developing oilseeds of California bay, *Umbellularia californica*. The bay thioesterase was subsequently purified by
10 Davies et al., (Arch. Biochem. Biophys. (1991) 290:37-45) which allowed the cloning of a corresponding cDNA which has been used to modify the triglyceride composition of plants (WO 91/16421 and WO 92/20236).

- Medium-chain thioesterases from *Cuphea hookeriana* and elm
15 which demonstrated activity on C8 and C10 substrates are described in WO 94/10288. Production of C16 fatty acids in transgenic plants by expression of Class II type thioesterase genes is described in WO 95/13390.

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DESCRIPTION OF THE FIGURES

Figure 1. The nucleic acid sequence and translated amino acid sequence of *Cuphea palustris* C14:0-ACP thioesterase cDNA clone MCT34 (CpFatB2) are provided.

- Figure 2. The nucleic acid sequence and translated amino
25 acid sequence of a nutmeg (*Myristica fragrans*) Class II type thioesterase, MYRF-1 (MfFatB2), having preferential activity on C14:0-ACP is provided.

- Figure 3. The nucleic acid sequence and translated amino acid sequence of a nutmeg (*Myristica fragrans*) Class II type
30 thioesterase, MYRF-2 (MfFatB1), having preferential activity on C14:0-ACP is provided.

- Figure 4. Nucleic acid and translated amino acid sequence of a PCR fragment containing the encoding region for the mature protein portion of a camphor Class II acyl-ACP thioesterase is
35 provided.

Figure 5. The nucleic acid sequence and translated amino acid sequence of an elm acyl-ACP thioesterase partial cDNA clone are provided.

Figure 6. The nucleic acid sequence of a *Cuphea hookeriana* CUPH-4 thioesterase cDNA clone, CMT13, is provided.

Figure 7. Nucleic acid sequence of an oleosin expression cassette is provided.

5 Figure 8. Mole % fatty acid composition data from single seeds of *Brassica* plants 3854-3 and 3854-11, expressing a nutmeg FatB thioesterase, are provided.

10 Figure 9. Mole % fatty acid composition data from single seeds of *Brassica* plants 5233-5 (Figure 9A) and 5233-6 (Figure 9B), expressing a camphor FatB thioesterase, are provided.

Figure 10. Mole % fatty acid composition data from single seeds of *Brassica* plants 3863-10, 3863-7, 3863-4, 3863-8, 3863-2 and 3863-5, expressing a *C. palustris* FatB thioesterase, are provided.

15 Figure 11. A graph of the C16 and C14 fatty acid compositions of seeds from *B. napus* plants transformed with C14 thioesterases from *C. palustris*, camphor and nutmeg is provided.

20 Figure 12. Mole % fatty acid composition data from pooled seeds of *Brassica napus* plants transformed with oleosin/*C. palustris* C14 thioesterase (pCGN3864) and oleosin/nutmeg C14 thioesterase (pCGN3857) constructs are provided.

SUMMARY OF THE INVENTION

25 By this invention, plant genes encoding acyl-ACP thioesterases having the ability to act on C14:0-ACP substrate to form C14:0 (myristate) are provided. Depending on the particular thioesterase employed, the production of myristate may be accompanied by the production of increased proportions
30 of other saturated fatty acids, such as C16 (palmitate) and C18 (stearate). The invention encompasses sequences which encode biologically active thioesterases from plants, as well as sequences which are to be used as probes, vectors for transformation or cloning intermediates. Biologically active
35 sequences are preferentially found in a sense orientation with respect to transcriptional regulatory regions found in various constructs. The instant invention pertains to the entire or portions of the genomic sequence or cDNA sequence and to the

thioesterase protein encoded thereby, including precursor or mature plant thioesterases.

Various plant genes encoding thioesterases having the ability to hydrolyze C14:0-ACP substrate are exemplified
5 herein, and may be obtained for example from *Cuphea* species, nutmeg and camphor. The exemplified plant thioesterase sequences may also be used to obtain other related plant thioesterase genes.

Of special interest are recombinant DNA constructs which
10 can provide for the transcription or transcription and translation (expression) of the disclosed protein sequences. In particular, constructs which are capable of transcription or transcription and translation in plant host cells are preferred. Such construct may contain a variety of regulatory
15 regions including transcriptional initiation regions obtained from genes preferentially expressed in plant seed tissue.

In a second aspect, this invention relates to the presence of such constructs in host cells, especially plant host cells, and to a method for producing proteins having C14 acyl-ACP
20 thioesterase activity in a host cell or progeny thereof via the expression of a construct in the cell. In a related aspect, this invention provides transgenic host cells which have an expressed protein having C14 acyl-ACP thioesterase activity therein.

25 In a different embodiment, this invention relates to methods of using a DNA sequence encoding a protein having hydrolysis activity on C14:0 acyl-ACP substrates for the modification of the proportion of fatty acids produced within a cell, especially plant cells. Plant cells having such a
30 modified fatty acid composition are also contemplated herein.

Of particular interest is the modification of the fatty acid composition of storage triglycerides in oilseed plants for increased proportion of C14:0 fatty acyl groups, and in some cases, increases in other saturated fatty acyl groups, such as
35 those having 16 and 18 carbons. In this manner, seeds with modified oils having novel fatty acyl compositions are produced. Such novel seeds and oils are also encompassed by the instant invention.

DETAILED DESCRIPTION OF THE INVENTION

A plant protein capable of hydrolyzing C14 acyl-ACP substrates for use in the instant invention includes any sequence of amino acids, peptide, polypeptide or protein which demonstrates the ability to catalyze the production of free fatty acid(s) from C14:0-ACP substrates under plant enzyme reactive conditions. By "enzyme reactive conditions" is meant that any necessary conditions are available in an environment (i.e., such factors as temperature, pH, lack of inhibiting substances) which will permit the enzyme to function. Such proteins having C14 hydrolysis activity are obtainable from various plant sources and will also demonstrate hydrolysis activity on fatty acyl-ACP of varying chain lengths, including such saturated fatty acids as palmitate (16:0) and in some cases, stearate (18:0).

Of particular interest in the instant application are plant acyl-ACP thioesterases which have hydrolysis activity primarily on C14:0-ACP substrates as compared to other acyl-ACP substrates, including medium- or long-chain acyl-ACP substrates. In this regard, thioesterase encoding sequences obtainable from *Cuphea palustris* are of particular interest in the instant invention. Other plant thioesterases having C14:0-ACP activity are also of interest, so long as the thioesterase demonstrates preferential activity on C14:0-ACP substrates, as compared to other medium-chain acyl-ACP substrates, i.e. those having carbon chain lengths of C8, C10 or C12. Thus, acyl-ACP thioesterases from nutmeg and camphor, which have substantial activity on C14:0-ACP substrates, as well as some activity on longer and other medium-chain substrates, are also encompassed by the instant invention. Thus, it is recognized that plant acyl-ACP thioesterases useful for C14 production may also demonstrate hydrolysis activity on longer chain acyl-ACP substrates, such as those having carbon chain lengths of C16 or C18.

In addition to the plant C14:0-ACP thioesterase sequences exemplified herein, acyl-ACP thioesterases from other plant species are also of interest in the instant invention. Target plant species for isolation of genes encoding thioesterase having activity on C14:0-ACP substrates include those which

have been reported to accumulate significant levels of C14 fatty acids, such as *Myristicaceae*, *Simarubaceae*, *Vochysiaceae*, and *Salvadoraceae*, and rainforest species of *Erisma*, *Picramnia* and *Virola*. For isolating C14:0-ACP thioesterase genes,
5 nucleic acid probes may be prepared from C14:0-ACP thioesterase sequences provided herein, or from other plant medium-chain acyl-ACP thioesterase sequences which have been described.

Plant thioesterases, including medium-chain plant thioesterases are described in WO 91/16421 (PCT/US91/02960), WO
10 92/20236 (PCT/US92/04332), WO 94/10288 (PCT/US93/10814), and WO 95/13390 (PCT/US94/13131) which are hereby incorporated by reference in their entirety. Analysis of the encoding sequences and translated amino acid sequences of a number of plant acyl-ACP thioesterases has demonstrated the existence of
15 two evolutionary classes of plant acyl-ACP thioesterases which are designated as "Class I" or "Fata" (for fatty acyl transferase type A) and "Class II" (or "FatB"). These classes are not a simple reflection of phylogenetic relationships of the various plants from which the thioesterase encoding
20 sequences were obtained. For example, a *Cuphea hookeriana* FataA clone (clone CLT7 in Figure 10 of WO 94/10288) is closely related to safflower FataA clones (sequences provided in Figure 4 of WO 92/20236). In contrast, a *Cuphea hookeriana* FatB clone (CUPH-1 clone in Figure 6 of WO 94/10288) is equally distant in
25 evolutionary relationship from the *Cuphea hookeriana* FataA clone and the safflower FataA clone.

Class I thioesterases have been found in mango (Fig.1), safflower, *Brassica campestris* and *Cuphea hookeriana*, which sequences are provided in USSN 07/949,102, filed September 21,
30 1992, now pending, and in WO 92/20236 and WO 94/10288. The plant Class I type thioesterases which have been described to date have preferential activity on longer chain acyl-ACP substrates, particularly 18:1-ACP. Class II thioesterases have been discovered, for example, in California bay, elm, *Cuphea*
35 *hookeriana*, *Arabidopsis thaliana* and camphor. The plant C14:0 acyl-ACP thioesterases described herein are also of the Class II type. All medium-chain preferring acyl-ACP thioesterases described to date, including those having activity on C14:0, are of the Class II type. Thus, additional plant acyl-ACP

thioesterases having activity on C14:0 substrates may be identified through sequence homology to medium-chain acyl-ACP thioesterases.

For example, a *C. palustris* C14 acyl-ACP thioesterase exemplified herein was obtained by screening a gene library with encoding sequences for medium-chain preferring acyl-ACP thioesterases from *Cuphea hookeriana*. Although the *C. hookeriana* gene sequences encode thioesterases having preferential activity on C8, C10 or C16 fatty acids, the substantial sequence homology within thioesterase genes in various *Cuphea* species allowed for detectable hybridization of the *C palustris* C14 clone to the *C hookeriana* gene probes. For hybridization of C14 thioesterases from plants other than *Cuphea* species, direct hybridization techniques may also be successful under low stringency conditions. For example, nutmeg C14:0-ACP thioesterase clones described herein were obtained by low stringency hybridization screening using a bay C12:0-ACP thioesterase gene fragment as probe. Thus, medium-chain acyl-ACP thioesterase genes from other plant species may be used to identify C14 acyl-ACP thioesterase genes. In addition, highly conserved regions have been identified in various plant medium-chain thioesterase amino acid sequences. Such regions find particular use in identification of additional medium-chain thioesterase genes, including those having preferential activity on C14:0-ACPs, for example by PCR amplification techniques.

As noted above, plants having significant presence of C14:0 fatty acids therein are preferred candidates to obtain naturally-derived C14:0 plant thioesterases. However, it should also be recognized that other plant sources which do not have a significant presence of C14:0 fatty acids may be screened as additional enzyme sources. For example, as discussed herein, a camphor acyl-ACP thioesterase gene was discovered to have preferential hydrolysis activity on C14:0-ACP substrates, with only minor activity on C12:0-ACP substrates, although analysis of camphor seed oil composition indicates significant levels of C12:0 fatty acyl groups and only low levels of C14 fatty acids. Thus, expression of medium-chain acyl-ACP thioesterases in *E. coli* may be used to

identify acyl-ACP thioesterases which find use in production of C14:0 fatty acids in transgenic plant seed oils.

Northern analysis of candidate plant acyl-ACP thioesterase genes may also be useful to identify those having activity on
5 C14:0 fatty acids. In *Cuphea hookeriana*, a clone, CUPH-1, which is expressed at low levels in various plant tissues has been demonstrated to have hydrolytic activity primarily on 16:0 acyl-ACP substrates. A related *C. hookeriana* thioesterase clone, CUPH-2, however, was demonstrated to be highly expressed
10 and seed specific. This CUPH-2 clone was found to have hydrolytic activity primarily on medium-chain acyl-ACP substrates, namely C8 and C10. Similarly, *C. hookeriana* CUPH-4 is highly expressed in a seed specific manner, and as demonstrated further in the Examples herein, may be used to
15 provide for increased production of C14 fatty acids in transformed host cells.

One skilled in the art will readily recognize that antibody preparations, nucleic acid probes (DNA and RNA) and the like may be prepared and used to screen and recover
20 "homologous" or "related" thioesterases from a variety of plant sources. For immunological screening methods, antibody preparations either monoclonal or polyclonal are utilized. For detection, the antibody is labeled using radioactivity or any one of a variety of second antibody/enzyme conjugate systems
25 that are commercially available. Examples of some of the available antibody detection systems are described by Oberfelder (*Focus* (1989) BRL Life Technologies, Inc., 11:1-5).

For nucleic acid screening methods, genomic or cDNA libraries prepared from a candidate plant source of interest
30 may be probed with conserved sequences from plant thioesterase to identify homologously related sequences. Homologous sequences are found when there is an identity of sequence, which may be determined upon comparison of sequence information, nucleic acid or amino acid, or through
35 hybridization reactions between a known thioesterase and a candidate source. Conservative changes, such as Glu/Asp, Val/Ile, Ser/Thr, Arg/Lys and Gln/Asn may also be considered in determining amino acid sequence homology. Amino acid sequences are considered homologous by as little as 25% sequence identity

between the two complete mature proteins. (See generally, Doolittle, R.F., *OF URFS and ORFS* (University Science Books, CA, 1986.)

Typically, a lengthy nucleic acid sequence may show as
5 little as 50-60% sequence identity, and more preferably at
least about 70% sequence identity, between the target sequence
and the given plant thioesterase of interest excluding any
deletions which may be present, and still be considered
related. When longer nucleic acid fragments (>100 bp) are
10 employed as probes, such as large cDNA fragments, one may
screen with low stringencies (for example 40-50°C below the
melting temperature of the probe) in order to obtain signal
from the target sample with 20-50% deviation, i.e., homologous
sequences. (See, Beltz, et al. *Methods in Enzymology* (1983)
15 100:266-285.).

Shorter probes are also useful in thioesterase gene
isolation techniques, and find particular applications in
polymerase chain reactions (PCR). As described in more details
in the following examples, medium-chain thioesterase gene
20 fragments may be obtained by PCR using primers to sequences
which are highly conserved in plant medium chain acyl-ACP
thioesterase protein sequences.

Using methods known to those of ordinary skill in the art,
a DNA sequence encoding a protein having hydrolytic activity on
25 C14:0-ACP substrate can be inserted into constructs which may
then be introduced into a host cell of choice for expression of
the enzyme, including plant cells for the production of
transgenic plants. Thus, potential host cells include both
prokaryotic and eukaryotic cells. A host cell may be
30 unicellular or found in a multicellular differentiated or
undifferentiated organism depending upon the intended use.
Cells of this invention may be distinguished by having a
protein having hydrolysis activity on C14:0 acyl-ACP substrates
foreign to the wild-type cell present therein, for example, by
35 having a recombinant nucleic acid construct encoding a plant
thioesterase therein.

Also, depending upon the host, the regulatory regions will
vary, including regions from viral, plasmid or chromosomal
genes, or the like. For expression in prokaryotic or

eukaryotic microorganisms, particularly unicellular hosts, a wide variety of constitutive or regulatable promoters may be employed. Among transcriptional initiation regions which have been described are regions from bacterial and yeast hosts, such as *E. coli*, *B. subtilis*, *Sacchromyces cerevisiae*, including genes such as beta-galactosidase, T7 polymerase, tryptophan E and the like.

For the most part, when expression in a plant host cell is desired, the constructs will involve regulatory regions (promoters and termination regions) functional in plants. The open reading frame, coding for the protein having hydrolytic activity on C14:0-ACP substrate will be joined at its 5' end to a transcription initiation regulatory region such as the wild-type sequence naturally found 5' upstream to a plant thioesterase structural gene. Numerous other transcription initiation regions are available which provide for a wide variety of constitutive or regulatable, e.g., inducible, transcription of the structural gene functions. Among transcriptional initiation regions used for plants are such regions associated with the structural genes such as for CaMV 35S and nopaline and mannopine synthases, or with napin, ACP promoters and the like. The transcription/translation initiation regions corresponding to such structural genes are found immediately 5' upstream to the respective start codons. If a particular promoter is desired, such as a promoter native to the plant host of interest or a modified promoter, i.e., having transcription initiation regions derived from one gene source and translation initiation regions derived from a different gene source, including the sequence encoding the plant thioesterase of interest, or enhanced promoters, such as double 35S CaMV promoters, the sequences may be joined together using standard techniques. For most applications desiring the expression of C14:0-ACP thioesterases in plants, the use of seed specific promoters is preferred.

For some applications, expression of other proteins in conjunction with expression of C14:0-ACP thioesterase may be desired. For example, as described in further detail in the following examples, expression of C14:0-ACP thioesterase results in C14 levels of up to 40 mole percent may be obtained,

analysis of the *sn*-1, 2 and 3 positions of the triglycerides indicates limited incorporation of C14 into the *sn*-2 position. Expression of a medium-chain preferring lysophosphatidic acid acyl transferase (LPAAT) in combination with a C14:0-ACP thioesterase results in increased incorporation of C14 into the *sn*-2 position. A plant medium-chain preferring LPAAT is described in international patent application number PCT/95/03997 (published as WO 95/27791), which is incorporated herein in its entirety.

When expression of the proteins of the instant invention is desired in plant cells, various plants of interest include, but are not limited to, rapeseed (Canola varieties, including low linolenic lines, and High Erucic Acid varieties), sunflower, safflower, cotton, *Cuphea*, soybean, peanut, coconut and oil palms, and corn. Depending on the method for introducing the recombinant constructs into the host cell, other DNA sequences may be required. Importantly, this invention is applicable to dicotyledons and monocotyledons species alike and will be readily applicable to new and/or improved transformation and regulation techniques.

In any event, the method of transformation is not critical to the instant invention; various methods of plant transformation are currently available. As newer methods are available to transform crops, they may be directly applied hereunder. For example, many plant species naturally susceptible to *Agrobacterium* infection may be successfully transformed via tripartite or binary vector methods of *Agrobacterium* mediated transformation. In addition, techniques of microinjection, DNA particle bombardment, electroporation have been developed which allow for the transformation of various monocot and dicot plant species.

The C14 fatty acids produced in the transgenic host cells of this invention are useful in various commercial applications, and will find particular use, for example, in the detergent industry. Oils containing varying amounts of C14 and C16 fatty acids essentially in the *sn*-1 and *sn*-3 positions may find use in food applications, such as for shortenings.

The following examples are provided by way of illustration and not by way of limitation.

EXAMPLES

Example 1 Acyl-ACP Thioesterase SequencesA. *Cuphea hookeriana*

5 DNA sequences corresponding to *Cuphea* thioesterase peptide regions are obtained by PCR using degenerate oligonucleotides designed from peptide fragments from conserved regions of plant thioesterases described in WO 92/20236. A forward primer, TECU9, contains 17 nucleotides corresponding to all possible
10 coding sequences for amino acids 176-181 of the bay and camphor thioesterase proteins. A reverse primer, TECU3A, contains 18 nucleotides corresponding to the complement of all possible coding sequences for amino acids 283-288 of the bay and camphor thioesterase proteins. In addition, the forward and reverse
15 primers contain *Bam*HI or *Xho*I restriction sites, respectively, at the 5' end, and the reverse primer contains an inosine nucleotide at the 3' end. The safflower, bay and camphor sequences diverge at two amino acid positions in the forward primer region, and at one amino acid residue in the reverse
20 primer region. The degeneracy of oligonucleotide primers is such that they could encode the safflower, bay and camphor sequences.

Polymerase chain reaction samples (100µl) are prepared using reverse transcribed *Cuphea hookeriana* RNA as template and
25 1µM of each of the oligonucleotide primers. PCR products are analyzed by agarose gel electrophoresis, and an approximately 300bp DNA fragment, the predicted size from the thioesterase peptide sequences, is observed. The DNA fragment, designated C93A (*Cuphea*) is isolated and cloned into a convenient plasmid
30 vector using the PCR-inserted *Bam*HI and *Xho*I restriction digest sites. DNA sequence of representative clones is obtained. Analysis of these sequences indicates that at least two different, but homologous *Cuphea hookeriana* cDNAs were amplified.

35 Total *Cuphea* RNA for cDNA library construction may be isolated from developing *Cuphea hookeriana* embryos by modifying the DNA isolation method of Webb and Knapp (*Plant Mol. Biol. Reporter* (1990) 8:180-195). Buffers include:

- REC: 50mM TrisCl pH 9, 0.7 M NaCl, 10 mM EDTA pH8,
0.5% CTAB.
- REC+: Add B-mercaptoethanol to 1% immediately prior
to use.
- 5 RECP: 50 mM TrisCl pH9, 10 mM EDTA pH8, and 0.5% CTAB
- RECP+: Add B-mercaptoethanol to 1% immediately prior
to use.

For extraction of 1 g of tissue, 10ml of REC+ and 0.5 g of
10 PVPP is added to tissue that has been ground in liquid nitrogen
and homogenized. The homogenized material is centrifuged for 10
min at 1200 rpm. The supernatant is poured through miracloth
onto 3ml cold chloroform and homogenized again. After
centrifugation, 12,000 RPM for 10 min, the upper phase is taken
15 and its volume determined. An equal volume of RECP+ is added
and the mixture is allowed to stand for 20 min. at room
temperature. The material is centrifuged for 20 min. at 10,000
rpm twice and the supernatant is discarded after each spin.
The pellet is dissolved in 0.4 ml of 1 M NaCl (DEPC) and
20 extracted with an equal volume of phenol/chloroform. Following
ethanol precipitation, the pellet is dissolved in 1 ml of DEPC
water. Poly (A) RNA may be isolated from this total RNA
according to Maniatis et al. (*Molecular Cloning: A Laboratory
Manual* (1982) Cold Springs Harbor, New York). cDNA libraries
25 may be constructed in commercially available plasmid or phage
vectors.

Thioesterase encoding fragments obtained by PCR as
described above are labeled and used to screen *Cuphea* cDNA
libraries to isolate thioesterase cDNAs. Preliminary DNA
30 sequence of a *Cuphea* cDNA clone TAA 342 is presented in Figure
X. Translated amino acid sequence of the *Cuphea* clone from the
presumed mature N-terminus (based on homology to the bay
thioesterase) is shown.

The sequence is preliminary and does not reveal a single
35 open reading frame in the 5' region of the clone. An open
reading frame believed to represent the mature protein sequence
is shown below the corresponding DNA sequence. The N-terminal
amino acid was selected based on homology to the bay
thioesterase protein.

Additional *Cuphea hookeriana* cDNA clones were obtained by screening a cDNA library prepared using a Uni-ZAP (Stratagene) phage library cloning system. The library was screened using radiolabeled TAA 342 DNA. The library was hybridized at 42°C
5 using 30% formamide, and washing was conducted at low stringency (room temperature with 1X SSC, 0.1% SDS). Numerous thioesterase clones were identified and DNA sequences determined. Three classes of *Cuphea* cDNA clones have been identified. The original TAA 342 clone discussed above is
10 representative of CUPH-1 type clones which have extensive regions of homology to other plant medium-chain preferring acyl-ACP thioesterases. Nucleic acid sequence and translated amino acid sequence of a CUPH-1 clone, CMT9, is shown in Figure 6 of WO 94/10288. The mature protein is believed to begin
15 either at or near the leucine at amino acid position 88, or the leucine at amino acid position 112. Northern analysis of RNA isolated from various *Cuphea hookeriana* plant tissues indicates that the CUPH-1 gene is expressed at a low level in all *Cuphea hookeriana* plant tissues examined.

20 A second class of *Cuphea* thioesterase cDNAs is identified as CUPH-2. These cDNAs also demonstrate extensive homology to other plant medium-chain acyl-ACP thioesterases. Expression of a representative clone, CMT7, in *E. coli* demonstrated that CUPH-2 clones encode a medium-chain preferring acyl-ACP
25 thioesterase protein having preferential activity towards C8 and C10 acyl-ACP substrates. DNA sequence and translated amino acid sequence of CMT7 is shown in Figure 7 of WO 94/10288.

Preliminary DNA sequence from the 5' end of an additional *Cuphea hookeriana* clone, CMT13, is shown in Figure 6 herein.
30 Although CMT13 demonstrates extensive sequence identity with CMT7, DNA sequence alignment reveals several gaps, which together total approximately 48 nucleotides, where the CMT13 clone is missing sequences present in the CMT7 clone. CMT13 is also referred to as a CUPH-4 clone. Northern analysis of RNA
35 isolated from various *Cuphea hookeriana* plant tissues indicates that CUPH-2 and CUPH-4 genes are highly expressed in developing seed tissues. Expression of the CUPH-2 and CUPH-4 clones in other *C. hookeriana* tissues, such as leaves, was not detected.

DNA sequence of an additional clone, CMT10, is shown in Figure 9 of WO 94/10288. CMT10 has greater than 90% sequence identity with CMT9, but less than the approximately 99% sequence identity noted in fragments from other CUPH-1 type clones. CMT10 is also referred to as a CUPH-5 type clone.

B. *Cuphea palustris*

Total RNA is isolated from developing seeds of *C. palustris* as described above for *C. hookeriana*. A lambda ZipLox (BRL; Gaithersburg, MD) cDNA library containing approximately 6×10^6 pfu is constructed from total RNA. Approximately 500,000 plaques from the unamplified library are screened using a mixed probe containing the thioesterase coding regions from *Cuphea hookeriana* CUPH-1 (CMT-9), CUPH-2 (CMT-7) and CUPH-5 (CMT-10). (DNA sequences of these clones are provided in WO 94/10288). Low stringency hybridization conditions are used: hybridization is conducted at room temperature in a solution of 30% formamide and 2X SSC (1X SSC = 0.15 M NaCl; 0.015 M Na citrate). Eighty two putative positive clones were identified, thirty of which were plaque purified.

The nucleic acid sequence and translated amino acid sequence of clone designated as MCT34 is provided in Figure 1. The translated amino acid sequence of this clone is approximately 80% identical to the sequence of a *Cuphea hookeriana* CUPH-4 clone (CMT-13 in Figure 8 of WO 94/10288).

C. Nutmeg (*Myristica fragrans*)

Total RNA is isolated from developing nutmeg seeds as described above for *Cuphea* species. A lambda Zap (Stratagene; La Jolla, CA) cDNA library is constructed from total RNA. A *Bam*HI/*Pst*I fragment of pCGN3822 containing approximately 900bp of a bay thioesterase C12 preferring acyl-ACP thioesterase encoding sequence (Figure 1 of WO 94/10288) is radiolabeled and used as a probe of the nutmeg cDNA library under the following hybridization conditions: overnight hybridization at 30°C in 50% formamide, 2X SSC, 5% dextran sulfate. The hybridized filters are washed at 30°C in 0.1% SSC, 0.1% SDS and autoradiographed. Five putative positive clones were identified, three of which contain the sequence shown in Figure 3, and are designated MYRF-2 or MfFatB1, and one of which contained the sequence shown in Figure 2, and which is

designated MYRF-1 or MfFatB2. Sequence of the other putative positive clone indicated that it did not encode an acyl-ACP thioesterase.

Sequence analysis of the MYRF-1 and MYRF-2 clones indicates that MYRF-1 is substantially a truncated version of MYRF-2, the initial proline residue of MYRF-1 corresponds to amino acid 97 of the MYRF-2 sequence. Another major difference in these clones is seen at the 3' end of the thioesterase encoding regions. The MYRF-1 clone lacks the TAG stop codon at nucleotides 1624-1626 of the MYRF-2 sequence, and thus the translated amino acid sequence of MYRF-1 extends into the MYRF-2 3' untranslated region until the next available in frame stop codon is reached (TGA at nucleotides 1087-1089 of MYRF-1).

D. Camphor (*Cinnamomum camphora*)

DNA sequence and translated amino acid sequence of a Class II camphor thioesterase encoding region generated by PCR is provided in Figure 5B of WO 92/20236. A DNA fragment containing the mature protein region of the camphor clone is obtained by PCR from reverse transcribed cDNA prepared using RNA from developing camphor embryos. Forward (sense) and reverse (antisense) PCR primers, #4164 and #4165, are prepared which contain sequences useful for cloning using the CLONEAMP™ system (GIBCO BRL; Gaithersburg, MD). Oligonucleotide 4164 contains a 20 nucleotide region corresponding to the camphor thioesterase encoding sequence of nucleotides 119-138 of the sequence in Figure 5B of WO 92/20236. Oligonucleotide 4165 contains a 20 nucleotide region complementary to the camphor thioesterase 3' untranslated sequence represented as nucleotides 1391-1410 of Figure 5B in WO 92/20236. The sequences of 4164 and 4165 are as follows:

#4164 5' CUACUACUACUATCGATACCATCTTTTCGGCTGCTGA 3'

#4165 5' CAUCAUCAUGAGCTCGCAAGAGAAAGAGCTTACAG 3'.

DNA sequence and translated amino acid sequence of a camphor PCR fragment obtained by PCR with 4164 and 4165 are provided in Figure 4. The sequence begins at the XbaI site located at the beginning of the mature protein encoding region of the camphor thioesterase.

Example 2 - Expression of C14:0 Acyl-ACP Thioesterases
in *E. coli*

A. *Cuphea palustris*

5 Constructs for expression of a *Cuphea palustris* acyl-ACP
thioesterase encoding sequence in *E. coli* are prepared. cDNA
clone MCT34 is used as template for a polymerase chain reaction
(PCR) to insert a *StuI* site 5' to the presumed mature protein
start site located at amino acid 108 of the sequence shown in
10 Figure 1. A forward primer for PCR, MCT34F1, contains DNA
sequence corresponding to nucleotides 437-454 of the *C.*
palustris sequence shown in Figure 1, as well as sequences for
insertion of *SphI* and *StuI* restriction digestion sites. An M13
sequencing primer referred to as "M13 Forward" is used for
15 priming the reverse, or antisense, reaction. Sequence of the
PCR primers are as follows:

MCT34F1 5' CUACUACUACUAGAATTCGCATGCAGGCCTATGCTTGACCGGAAATCT 3'
M13 Forward 5' GTTTTCCCAGTCACGAC 3'.

20

The resulting PCR product is cloned as a *StuI/XbaI*
fragment into pUC118, resulting in clone MCT34LZ, which
provides for expression of the *C. palustris* thioesterase in *E.*
coli as a *lacZ* fusion protein.

25 An additional construct for expression of the *C. palustris*
thioesterase cDNA clone MCT34 in *E. coli* is prepared using a
Qiagen (Chatsworth, CA) pQE vector which provides for high
level expression and protein purification capability through a
histidine tag. The DNA product resulting from PCR using the
30 MCT34F1 and M13 Forward primers described above, is digested
with *SphI* and *SnaBI* and cloned into *SphI* and *SmaI* digested
pQE30 (Qiagen), resulting in MCT34HT.

MCT34LZ is transformed into *E. coli fadD*, an *E. coli*
mutant which lacks medium-chain specific acyl-CoA synthetase
35 (Overath et al., *Eur. J. Biochem* (1969) 7:559-574) for analysis
of lipid composition. Cells containing the thioesterase
construct, and a similar culture of control cells are grown at
30°C to an OD₆₀₀ of ~0.5. Induction of the thioesterase
expression may be achieved by the addition of IPTG to 0.2 to

0.4 mM followed by further growth for 30 to 120 minutes. For slow growing cultures, longer growth periods may be required following addition of IPTG. A 4.5ml sample of the *E. coli* cells is transferred into a 15ml glass vial with a teflon-lined cap. 100µl of a 1mg/ml standards solution containing 1mg/ml each of C11:0 free fatty acid, C15:0 free fatty acid, and C17:0 TAG in 1:1 chloroform/methanol is added to the sample, followed by addition of 200µl of glacial acetic acid and 10ml of 1:1 chloroform/methanol. The samples are vortexed to mix thoroughly and centrifuged for 5 minutes at 1000rpm for complete phase separation. The lower (chloroform) phase is carefully removed and transferred to a clean flask appropriate for use in a rotary evaporator (Rotovap). The sample is evaporated to near dryness. As medium-chain fatty acids appear to evaporate preferentially after solvent is removed, it is important to use just enough heat to maintain the vials at room temperature and not completely remove the chloroform. The liquid residue is measured and transferred to a 2ml glass vial with a Teflon cap. The vial used in the rotary evaporator is washed with chloroform/methanol, and the chloroform/methanol sample is pooled with the liquid residue (total volume of 600µl).

For analysis of total fatty acids, a 100µl aliquot of the sample is methanolized by adding 1 ml of 5% sulfuric acid in methanol, transferring the samples to a 5ml vial, and incubating the sample in a 90°C water bath for 2 hours. The sample is allowed to cool, after which 1ml of 0.9% NaCl and 300µl of hexane are added. The sample is vortexed to mix thoroughly and centrifuged at 1000rpm for 5 minutes. The top (hexane) layer is carefully removed and placed in a plastic autosampler vial with a glass cone insert, followed by capping of the vial with a crimp seal.

For analysis of free fatty acids, the following TLC procedure for separation of free fatty acids from phospholipids (Cho and Cronan (1994) *J. Bacterial.* 1793-1795) is applied prior to methanolysis as described above. A 100µl aliquot of the rotary evaporator residue and wash solution described above is applied to two lanes (50µl/lane) of a silica-G TLC plate. The plates are developed in petroleum ether/ether/acetic acid

(70/30/2, v/v) for approximately 15-20 minutes. The phospholipids remain at the origin, while the neutral lipids migrate close to the solvent front. Lipids are stained with iodine very briefly, marked and the silica from the marked areas transferred to Teflon-capped 2ml tubes. The respective areas from the two lanes are pooled, and the samples are methanolized as described above.

Samples are analyzed by gas-liquid chromatography (GC) using a temperature program to enhance the separation of components having 10 or fewer carbons. The temperature program used provides for a temperature of 140°C for 3 minutes, followed by a temperature increase of 5°C/minute until 230°C is reached, and 230°C is maintained for 11 minutes. Samples are analyzed on a Hewlett-Packard 5890 (Palo Alto, CA) gas chromatograph. Fatty acid content calculations are based on the internal standards. Results are presented in Table 1 below.

TABLE 1

Free Fatty Acids (nmol/ml) in *E. coli* (*fadD*)

<u>Strain</u>	<u>12:0</u>	<u>14:0</u>	<u>14:1</u>	<u>16:0</u>	<u>16:1</u>	<u>18:1</u>
Control	1.87	0.54	0.0	1.70	0.0	0.0
MCT34LZ	2.41	8.83	19	2.96	0.0	0.0

The above results demonstrate a substantial increase in the production of 14:0 and 14:1 fatty acids in cells transformed with the *C. palustris* MCT34LZ clone.

B. *C. hookeriana* CUPH-4

A construct for expression of *C. hookeriana* CUPH-4 thioesterase in *E. coli* as a *lacZ* fusion is also prepared using PCR and cloning techniques such as described above for preparation of *C. palustris* constructs.

C. Nutmeg

Constructs for expression of two nutmeg (*Myristica fragrans*) Class II type thioesterases, MYRF-1 (MfFatB2) and MYRF-2 (MfFatB1), in *E. coli* as *lacZ* fusion proteins are prepared. MfFatB1 and MfFatB2 are digested with *SalI* and *XhoI*

to excise the clone fragments containing the thioesterase encoding sequence from amino acid 131 of the MfFatB1 sequence (Figure 3), or amino acid 35 of the MfFatB2 sequence (Figure 2), through the 3' ends of the cDNA clones. The excised

5 thioesterase encoding fragments are inserted into *SalI* digested pUC8 resulting in pCGN3856 (MfFatB1) and pCGN3855 (MfFatB2). These constructs encode *lacZ* fusions of the approximate mature thioesterase protein sequence (amino acid 130 of the MfFatB1 preprotein was selected as the mature protein N-terminus by

10 homology to bay thioesterase protein).

The fusion proteins are expressed in *fad⁺* and *fadD* strains of *E. coli* K12. Analysis of total fatty acids in liquid cultures of MYRF-1 and MYRF-2 transformed K27(*fadD*) after overnight growth at 30°C are provided in Table 2 below.

15 D. Camphor

The camphor PCR fragment described above is cloned into a pAMP vector resulting in pCGN5219. pCGN5219 is digested with *XbaI* and *SalI* and the resulting camphor thioesterase fragment is cloned into *XbaI* and *SalI* digested pBCSK+ (Stratagene),

20 resulting in pCGN5220. pCGN5220 is used to transform *E. coli fadD* for analysis of lipid composition as described above. Results of these analyses are provided in Table 2 below.

TABLE 2

Total Fatty Acids (nmol/ml) in *E. coli* (*fadD*)

Strain	12:0	14:0	14:1	16:0	16:1	18:1
Control	3	19	2	141	59	42
MYRF-1	19	277	19	121	299	54
35 MYRF-2	32	240	31	47	296	17
CINC-1	99	195	204	43	102	26
CUPH-4	3	217	0	277	107	112

40 In comparison to the control, 14:0 and 16:1 fatty acids are drastically elevated for the nutmeg, camphor and *C. hookeriana* clones. Increases in 12:0 and 14:1 are also observed with the nutmeg and camphor clones, and increases in

16:0 and 18:1 are also seen with the *C. hookeriana* CUPH-4 clone.

E. Assay for Thioesterase Activity

For thioesterase activity assays, *E. coli* cells containing the acyl-ACP thioesterase constructs, and a similar culture of control cells are grown at 30°C to an OD₆₀₀ of ~0.5. Induction of thioesterase expression in *lacZ* fusion constructs may be achieved by the addition of IPTG to 0.4 mM followed by 1 or 2 hours further growth. For slow growing cultures, longer growth periods may be required following addition of IPTG.

A ten-ml aliquot of each culture (containing cells plus the culture medium) is assayed for specific activity towards various carbon chain length acyl-ACP substrates as follows. Cells are harvested by centrifugation, resuspended in 0.5 ml assay buffer and lysed by sonication. Cell debris may be removed by further centrifugation. The supernatant is then used in thioesterase activity assays as per Pollard et al., *Arch. Biochem & Biophys.* (1991) 281:306-312. Results of thioesterase activity assays on Cuphea, nutmeg and camphor thioesterase clones using 8:0, 10:0, 12:0, 14:0, 16:0, 18:0 and 18:1 acyl-ACP substrates are provided in Table 3 below. Results are presented as relative activity of the thioesterase expressing cells compared to control cells.

TABLE 3

Relative Activity (TE/Control)

Strain	8:0	10:0	12:0	14:0	16:0	18:0	18:1
MCT34HT	0.9	0.8	1.0	42.8	21.8	1.5	
MYRF-1	1.1	1.4	1.8	13.6	13.3	5.5	13.6
MYRF-2	0.9	0.9	0.8	4.2	6.6	2.8	10.9
CINC-1		1.3	1.9	8.9	2.0	1.1	1.1

Substantial increases in the hydrolysis activity on 14:0 and 16:0 relative to the control cells are observed with *C. palustris* MCT34HT transformed cells. Cells transformed with the nutmeg MYRF-1 and MYRF-2 clones also demonstrate substantial increases in activity on 14:0 and 16:0 substrates,

as well as less substantial increases with 18:0 and 18:1. Expression of the camphor CINC-1 clone results mainly in increased activity on 14:0, although a lesser increase in 16:0 hydrolysis activity is also observed.

5

Example 3 - Constructs for Plant Transformation

A. Napin Expression Cassette

A napin expression cassette, pCGN1808, is described in copending US Patent Application serial number 07/742,834 which is incorporated herein by reference. pCGN1808 is modified to contain flanking restriction sites to allow movement of only the expression sequences and not the antibiotic resistance marker to binary vectors. Synthetic oligonucleotides containing *KpnI*, *NotI* and *HindIII* restriction sites are annealed and ligated at the unique *HindIII* site of pCGN1808, such that only one *HindIII* site is recovered. The resulting plasmid, pCGN3200 contains unique *HindIII*, *NotI* and *KpnI* restriction sites at the 3'-end of the napin 3'-regulatory sequences as confirmed by sequence analysis.

The majority of the napin expression cassette is subcloned from pCGN3200 by digestion with *HindIII* and *SacI* and ligation to *HindIII* and *SacI* digested pIC19R (Marsh, et al. (1984) *Gene* 32:481-485) to make pCGN3212. The extreme 5'-sequences of the napin promoter region are reconstructed by PCR using pCGN3200 as a template and two primers flanking the *SacI* site and the junction of the napin 5'-promoter and the pUC backbone of pCGN3200 from the pCGN1808 construct. The forward primer contains *ClaI*, *HindIII*, *NotI*, and *KpnI* restriction sites as well as nucleotides 408-423 of the napin 5'-sequence (from the *EcoRV* site) and the reverse primer contains the complement to napin sequences 718-739 which include the unique *SacI* site in the 5'-promoter. The PCR was performed using in a Perkin Elmer/Cetus thermocycler according to manufacturer's specifications. The PCR fragment is subcloned as a blunt-ended fragment into pUC8 (Vieira and Messing (1982) *Gene* 19:259-268) digested with *HincII* to give pCGN3217. Sequenced of pCGN3217 across the napin insert verifies that no improper nucleotides were introduced by PCR. The napin 5-sequences in pCGN3217 are ligated to the remainder of the napin expression cassette by

digestion with *Cla*I and *Sac*I and ligation to pCGN3212 digested with *Cla*I and *Sac*I. The resulting expression cassette pCGN3221, is digested with *Hind*III and the napin expression sequences are gel purified away and ligated to pIC20H (Marsh, *supra*) digested with *Hind*III. The final expression cassette is pCGN3223, which contains in an ampicillin resistant background, essentially identical 1.725 napin 5' and 1.265 3' regulatory sequences as found in pCGN1808. The regulatory regions are flanked with *Hind*III, *Not*I and *Kpn*I restriction sites and unique *Sal*I, *Bgl*II, *Pst*I, and *Xho*I cloning sites are located between the 5' and 3' noncoding regions.

B. Oleosin Expression Cassette

A cassette for cloning of sequences for transcription under the regulation of 5' and 3' regions from an oleosin gene may be prepared. Sequence of a *Brassica napus* oleosin gene is provided by Lee and Huang (*Plant Phys.* (1991) 96:1395-1397). Primers to the published sequence are used in PCR reactions to obtain the 5' and 3' regulatory regions of an oleosin gene from *Brassica napus* cv. Westar. Two PCR reactions were performed, one to amplify approximately 950 nucleotides immediately upstream of the ATG start codon for the oleosin gene, and one to PCR amplify approximately 600 bp including and downstream of the TAA stop codon for the oleosin gene. The PCR products were cloned into plasmid vector pAMP1 (BRL) according to manufacturer's protocols to yield plasmids pCGN7629 which contains the oleosin 5' flanking region and pCGN7630 which contains the 3' flanking region. The PCR primers included convenient restriction sites for cloning the 5' and 3' flanking regions together into an expression cassette. A *Pst*I fragment containing the 5' flanking region from pCGN7629 was cloned into *Pst*I digested pCGN7630 to yield plasmid pCGN7634. The *Bss*HII (New England BioLabs) fragment from pCGN7634, which contains the entire oleosin expression cassette was cloned into *Bss*HII digested pBCSK+ (Stratagene) to provide the oleosin cassette in a plasmid, pCGN7636. Sequence of the oleosin cassette in pCGN7636 is provided in Figure 7. The oleosin cassette is flanked by *Bss*HII, *Kpn*I and *Xba*I restriction sites, and contains *Sal*I, *Bam*HI and *Pst*I sites for insertion of wax

synthase, reductase, or other DNA sequences of interest between the 5' and 3' oleosin regions.

C. *C. palustris* Acyl-ACP Thio sterase Expression Constructs
Constructs for expression of *C. palustris* thioesterase

- 5 cDNA clone MCT34 in plant seeds under the regulatory control of napin and oleosin regulatory regions are prepared as follows. The thioesterase encoding region from MCT34 is obtained by PCR amplification using oligonucleotides for insertion of a *Sal*I site 5' to the ATG start codon, and an *Nsi*I site immediately 3' to the MCT34 translation stop codon. The oligonucleotide primers for PCR contained the *Sal*I site (CpMet-1 forward primer) and the *Nsi*I site (CpStop-1 reverse primer). In addition, the primers contain "CAU" (forward primer) and "CUA" (reverse primer) repeat sequences for cloning using the
- 10 to the MCT34 translation stop codon. The oligonucleotide primers for PCR contained the *Sal*I site (CpMet-1 forward primer) and the *Nsi*I site (CpStop-1 reverse primer). In addition, the primers contain "CAU" (forward primer) and "CUA" (reverse primer) repeat sequences for cloning using the
- 15 CLONEAMP™ system. Sequence of the PCR primers is as follows:

CpMet-1 5' CAUCAUCAUCAUGTCGACAAACATGGTGGCTGCCGAG 3'

CpStop-1 5' CUACUACUACUAATGCATTACTAAGATATAGAGTTTCCATTTG 3'.

- 20 The resulting PCR product is cloned into pAMP and the DNA sequence determined to verify the PCR products.

The *C. palustris* thioesterase pAMP clone (pCGN3860) is digested with *Sal*I and *Nsi*I and the thioesterase encoding fragment isolated and cloned into *Sal*I/*Pst*I digested pCGN3223 (napin expression cassette) or pCGN7636 (oleosin expression cassette), resulting in pCGN3861 and pCGN3862, respectively.

25 (napin expression cassette) or pCGN7636 (oleosin expression cassette), resulting in pCGN3861 and pCGN3862, respectively.

Binary vectors for plant transformation with the *C. palustris* expression constructs are prepared by digestion of pCGN3861 and pCGN3862 with *Asp*718 and insertion of the resulting fragments into *Asp*718 digested pCGN1578 (McBride et al. (1990) *Plant Mol. Biol.* 14:269-276), resulting in pCGN3863 and pCGN3864, respectively.

30 resulting fragments into *Asp*718 digested pCGN1578 (McBride et al. (1990) *Plant Mol. Biol.* 14:269-276), resulting in pCGN3863 and pCGN3864, respectively.

D. Nutmeg Acyl-ACP Thioesterase Expression Construct

- Constructs for expression of nutmeg thioesterase cDNA clone MfFatB1 (pCGN3856 or MYRF-2) in plant seeds under the regulatory control of napin and oleosin regulatory regions are prepared as follows. The thioesterase encoding region from MfFatB1 is obtained by PCR amplification using oligonucleotides for insertion of a *Bam*HI site 5' to the ATG start codon, and an
- 35 clone MfFatB1 (pCGN3856 or MYRF-2) in plant seeds under the regulatory control of napin and oleosin regulatory regions are prepared as follows. The thioesterase encoding region from MfFatB1 is obtained by PCR amplification using oligonucleotides for insertion of a *Bam*HI site 5' to the ATG start codon, and an

*Xho*I site 3' to the *MfFatB1* translation stop codon. The oligonucleotide primers for PCR contained the *Bam*HI site (forward or sense primer) and the *Xho*I site (reverse or antisense primer). In addition, the primers contain "CAU" (forward primer) and "CUA" (reverse primer) repeat sequences for cloning using the CLONEAMP™ system. Sequence of the PCR primers is as follows:

10 Sense 5' CAUCAUCAUGGATCCCTCATCATGGTTGCCACATCTGC 3'
 Antisense 5' CUACUACUACUACTCGAGTTACATTTTGGCTATGC 3'.

The resulting PCR product is cloned into pAMP and the DNA sequence determined to verify the PCR products.

15 The nutmeg thioesterase pAMP clone (TA431) is digested with *Xho*I and partially digested with *Bam*HI. The thioesterase encoding fragment is isolated (1.3kb band) and cloned into *Bgl*III/*Xho* digested pCGN3223 (napin expression cassette), resulting in pCGN3868. A binary vector for plant transformation with the nutmeg expression construct is prepared
20 by digestion of pCGN3868 with *Asp*718, and insertion of the resulting napin 5'/nutmeg TE/ napin 3' fragment (4.2kb) into pCGN1578PASS at the *Asp*718 site. [pCGN1578PASS is prepared from pCGN1578 (McBride et al., supra) by substitution of the pCGN1578 polylinker region with a polylinker region containing
25 the following restriction sites: *Asp*718, *Asc*, *Pac*, *Swa*, *Sse* and *Hind*III.] The resulting construct, pCGN3854, is used for plant transformation for production of C14 fatty acids.

30 A construct for expression of the nutmeg thioesterase under the regulatory control of an oleosin promoter is prepared as follows. pCGN3868 (napin 5'/nutmeg TE/napin 3' expression construct described above) is digested with *Sal*I and *Eco*RV, and the resulting fragment, containing the nutmeg thioesterase encoding region joined in the 5' to 3' orientation to the napin 3' regulatory region, is inserted into *Sal*I and *Eco*RV digested
35 pCGN7636 (oleosin expression cassette described above). The resulting construct, pCGN3858, contains an oleosin 5'/nutmeg TE/ napin 3'/oleosin 3' construct. pCGN3858 is digested with *Asp*718 and partially digested with *Bam*HI to produce an ~2.6kb fragment containing the oleosin 5', nutmeg thioesterase

encoding region, and ~320 nucleotides of the napin 3' regulatory region. The 2.6kb fragment is cloned into Asp718/BamHI digested pCGN1578, resulting in pCGN3857, a binary vector for plant transformation and expression of the nutmeg

5 thioesterase.

E. Camphor Acyl-ACP Thioesterase Expression Construct

A construct for expression of camphor thioesterase under the regulatory control of a napin promoter is described. A transit peptide encoding sequence for bay thioesterase is

10 obtained by digestion of pCGN3826 (bay C12 preferring acyl-ACP thioesterase clone described in WO 92/20236) with XbaI and SalI generating a DNA fragment having a plasmid vector backbone and the bay transit peptide encoding sequence (XbaI site is at beginning of mature bay protein encoding region). pCGN5220

15 (Example 2D) is digested with XbaI and SalI to obtain the camphor mature TE encoding region. The pCGN5220 and pCGN3826 SalI/XbaI fragments are ligated to produce pCGN5231. pCGN5231 is digested with BamHI and SalI, and the resulting bay transit::camphor mature encoding fragment is inserted into

20 BglIII/XhoI digested pCGN3223 (napin expression cassette), resulting in pCGN5232. pCGN5232 was digested with NotI and, with Klenow to produce blunt ends, and the resulting napin 5'/bay transit::camphor mature/napin 3' fragment is inserted into HindIII digested and Klenow-blunted pCGN1578. The

25 resulting construct, pCGN5233, is a binary vector for plant transformation and expression of camphor thioesterase.

Example 4 Plant Transformation

A. Brassica Transformation

30 Brassica species may be transformed as reported by Radke et al. (*Plant Cell Reports* (1992) 11:499-505; *Theor. Appl. Genet.* (1988) 75:685-694), or as described in detail below.

Brassica napus seeds are soaked in 95% ethanol for 2 min. surface sterilized in a 1.0% solution of sodium hypochlorite

35 containing a drop of Tween 20 for 45 min., and rinsed three times in sterile, distilled water. Seeds are then plated in Magenta box s with 1/10th concentration of Murashige minimal organics medium (Gibco; Grand Island, NY) supplemented with pyridoxine (50µg/l), nicotinic acid (50µg/l), glycine

(200 μ g/l), and 0.6% Phytagar (Gibco) pH 5.8. Seeds are germinated in a Percival chamber at 22°C. in a 16 h photoperiod with cool fluorescent and red light of intensity approximately 65 μ Einsteins per square meter per second (μ Em⁻²S⁻¹).

- 5 Hypocotyls are excised from 5-7 day old seedlings, cut into pieces approximately 4mm in length, and plated on feeder plates (Horsch et al., *Science* (1985) 227:1229-1231). Feeder plates are prepared one day before use by plating 1.0ml of a tobacco suspension culture onto a petri plate (100x25mm)
- 10 containing about 30ml MS salt base (Carolina Biological, Burlington, NC) 100mg/l inositol, 1.3mg/l thiamine-HCl, 200mg KH₂PO₄ with 3% sucrose, 2,4-D (1.0mg/l), 0.6% w/v Phytagar, and pH adjusted to 5.8 prior to autoclaving (MS 0/1/0 medium). A sterile filter paper disc (Whatman 3mm) is placed on top of the
- 15 feeder layer prior to use. Tobacco suspension cultures are subcultured weekly by transfer of 10ml of culture into 100ml fresh MS medium as described for the feeder plates with 2,4-D (0.2mg/l), Kinetin (0.1mg/l). In experiments where feeder cells are not used hypocotyl explants are cut and placed onto a
- 20 filter paper disc on top of MS0/1/0 medium. All hypocotyl explants are preincubated on feeder plates for 24 h. at 22°C in continuous light of intensity 30 μ Em⁻²S⁻¹ to 65 μ Em⁻²S⁻¹.

- Single colonies of *A. tumefaciens* strain EHA 101 containing a binary plasmid are transferred to 5ml MG/L broth
- 25 and grown overnight at 30°C. Hypocotyl explants are immersed in 7-12ml MG/L broth with bacteria diluted to 1x10⁸ bacteria/ml and after 10-25 min. are placed onto feeder plates. Per liter MG/L broth contains 5g mannitol, 1g L-Glutamic acid or 1.15g sodium glutamate, 0.25g KH₂PO₄, 0.10g NaCl, 0.10g MGSO₄·7H₂O,
- 30 1mg biotin, 5g tryptone, and 2.5g yeast extract, and the broth is adjusted to pH 7.0. After 48 hours of co-incubation with *Agrobacterium*, the hypocotyl explants are transferred to B5 0/1/0 callus induction medium which contains filter sterilized carbenicillin (500mg/l, added after autoclaving) and kanamycin
- 35 sulfate (Boehringer Mannheim; Indianapolis, IN) at concentrations of 25mg/l.

After 3-7 days in culture at 65 μ Em⁻²S⁻¹ continuous light, callus tissue is visible on the cut surface and the hypocotyl explants are transferred to shoot induction medium, B5BZ (B5

salts and vitamins supplemented with 3mg/l benzylaminopurine, 1mg/l zeatin, 1% sucrose, 0.6% Phytagar and pH adjusted to 5.8). This medium also contains carbenicillin (500mg/l) and kanamycin sulfate (25mg/l). Hypocotyl explants are subcultured
5 onto fresh shoot induction medium every two weeks.

Shoots regenerate from the hypocotyl calli after one to three months. Green shoots at least 1cm tall are excised from the calli and placed on medium containing B5 salts and vitamins, 1% sucrose, carbenicillin (300mg/l), kanamycin
10 sulfate (50mg/l) and 0.6% w/v Phytagar). After 2-4 weeks shoots which remain green are cut at the base and transferred to Magenta boxes containing root induction medium (B5 salts and vitamins, 1% sucrose, 2mg/l indolebutyric acid, 50mg/l kanamycin sulfate and 0.6% Phytagar). Green rooted shoots are
15 tested for thioesterase activity.

B. *Arabidopsis* Transformation

Transgenic *Arabidopsis thaliana* plants may be obtained by *Agrobacterium*-mediated transformation as described by Valverkens et al., (*Proc. Nat. Acad. Sci.* (1988) 85:5536-5540).
20 Constructs are transformed into *Agrobacterium* cells, such as of strain EHA101 (Hood et al., *J. Bacteriol* (1986) 168:1291-1301), by the method of Holsters et al. (*Mol. Gen. Genet.* (1978) 163:181-187).

C. Peanut Transformation

25 DNA sequences of interest may be introduced as expression cassettes, comprising at least a promoter region, a gene of interest, and a termination region, into a plant genome via particle bombardment as described in European Patent Application 332 855 and in co-pending application USSN
30 07/225,332, filed July 27, 1988.

Briefly, tungsten or gold particles of a size ranging from 0.5 μ M-3 μ M are coated with DNA of an expression cassette. This DNA may be in the form of an aqueous mixture or a dry DNA/particle precipitate.

35 Tissue used as the target for bombardment may be from cotyledonary explants, shoot meristems, immature leaflets, or anthers.

The bombardment of the tissue with the DNA-coated particles is carried out using a Biolistics™ particle gun

(Dupont; Wilmington, DE). The particles are placed in the barrel at variable distances ranging from 1cm-14cm from the barrel mouth. The tissue to be bombarded is placed beneath the stopping plate; testing is performed on the tissue at distances up to 20cm. At the moment of discharge, the tissue is protected by a nylon net or a combination of nylon nets with mesh ranging from 10 μ m to 300 μ m.

Following bombardment, plants may be regenerated following the method of Atreya, et al., (*Plant Science Letters* (1984) 34:379-383). Briefly, embryo axis tissue or cotyledon segments are placed on MS medium (Murashige and Skoog, *Physio. Plant.* (1962) 15:473) (MS plus 2.0 mg/l 6-benzyladenine (BA) for the cotyledon segments) and incubated in the dark for 1 week at 25 \pm 2°C and are subsequently transferred to continuous cool white fluorescent light (6.8 W/m²). On the 10th day of culture, the plantlets are transferred to pots containing sterile soil, are kept in the shade for 3-5 days and finally moved to greenhouse.

The putative transgenic shoots are rooted. Integration of exogenous DNA into the plant genome may be confirmed by various methods known to those skilled in the art.

Example 5 - Analysis of Transgenic Plants

A. Nutmeg (MYRF-2) Expression Construct

Mature seeds were harvested from transgenic *Brassica napus* plants (a QL01 derived low linolenic variety) containing pCGN3854, a construct for expression of nutmeg thioesterase clone MYRF-2 under the regulatory control of a napin promoter, and analyzed to determine mole percent fatty acid composition. Results are presented in Table 4 below.

TABLE 4

Plant	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3
3854-1	0.00	0.26	0.30	13.50	22.10	0.49	4.84	37.62	16.26	1.96
3854-2	0.00	0.42	0.26	14.91	29.05	0.52	6.87	25.76	17.73	1.70
3854-3	0.00	0.27	0.43	21.73	30.90	0.43	6.48	19.54	15.85	1.62
3854-4	0.00	0.33	0.28	15.24	26.89	0.51	6.28	29.61	16.33	1.84

C14 fatty acyl groups are present in all four transgenic plants analyzed, with levels of C14 ranging from 13.5 to 21.73 mole perc nt. An even greater increase in C16 levels is observed, with ratios of C16 to C14 fatty acids ranging up to approximately 2:1. Generally, the C16/C14 ratio decreases with increasing C14 content, with ratios as low as approximately 1.3:1 being observed. A graph of the C14 and C16 levels in these transgenic plant seeds is provided in Figure 11. Background levels of C14 in non-transformed control plants are approximately 0.1 mole percent. Levels of C16 in non-transformed seeds of QL01 are approximately 4 mole percent. Single seeds from transformant 3854-3 are dissected for half seed lipid analysis. Results from these analyses are presented in Table 5 below.

TABLE 5

NO.	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3
1	0.00	2.31	0.40	19.11	29.78	0.36	6.63	22.69	14.08	1.46
2	0.00	1.84	0.37	20.26	30.45	0.44	5.76	19.30	17.49	1.51
3	0.00	1.53	0.37	16.87	29.24	0.49	8.11	25.66	13.06	1.44
4	0.00	2.39	0.44	20.82	29.96	0.58	6.02	18.47	16.78	1.68
5	0.00	2.91	0.43	19.66	30.16	0.62	6.71	23.12	12.43	1.48
6	0.00	2.01	0.40	18.52	29.50	0.36	6.99	23.49	14.01	1.67
7	0.00	4.02	0.51	23.04	29.94	0.25	5.30	17.16	16.13	1.75
8	0.00	3.13	0.38	18.03	27.87	0.58	6.09	25.51	14.31	1.51
9	0.00	3.00	0.44	21.23	29.19	0.63	5.68	17.58	18.34	1.85
12	0.00	2.52	0.34	17.80	28.93	0.38	6.73	23.62	15.11	1.53
13	0.00	2.56	0.45	21.48	30.59	0.49	6.02	18.43	16.02	1.48
14	0.00	2.19	0.39	18.40	30.48	0.47	7.44	23.39	12.68	1.42
15	0.00	1.88	0.28	15.17	28.81	0.44	7.73	28.03	12.94	1.35
16	0.00	2.10	0.38	19.83	30.34	0.43	6.23	20.33	15.95	1.33
17	0.00	2.44	0.42	18.73	28.89	0.60	7.21	22.26	14.83	1.68
18	0.00	2.77	0.45	20.32	29.55	0.47	6.55	21.93	13.93	1.46
19	0.00	3.37	0.40	17.72	27.95	0.48	6.38	24.22	14.01	2.01
20	0.00	2.40	0.36	19.72	29.92	0.50	6.72	19.79	16.10	1.52

Additional single seed fatty acid composition data (mole percent fatty acids) from 3854-3 and 3854-11 are presented in Figure 8. These data indicate C14 levels of up to 23% and C16 levels of up to 38% are obtained by expression of nutmeg thioesterase. In addition, smaller increases in 18:0 fatty acid levels are observed, with levels increasing from 1 mole

percent in non-transformed seeds of QL01 to levels of up to 9 mole percent in the transgenic seeds. Total saturated fatty acid levels in the transgenic seeds range from approximately 55 to 60 mole percent.

5 B. Camphor Expression Construct

Mature seeds were harvested from transgenic *Brassica napus* plants containing pCGN5233, a construct for expression of camphor thioesterase clone CINC-1 under the regulatory control of a napin promoter, and analyzed to determine mole percent fatty acid composition. Results are presented in Table 6 below.

TABLE 6

Plant	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3
5233-1	0.00	0.84	0.87	6.93	9.64	0.95	1.51	41.35	21.47	14.99
5233-2	0.00	0.85	0.38	3.83	8.41	0.70	1.43	46.33	21.71	14.98
5233-4	0.00	0.96	1.33	11.46	11.69	1.06	1.16	31.07	23.54	16.26
5233-5	0.00	0.69	0.93	8.77	10.38	0.90	1.48	42.22	19.88	13.41
5233-6	0.00	0.69	1.29	11.38	10.98	0.83	1.54	40.75	18.32	12.98
5233-7	0.00	0.70	0.36	4.44	8.57	0.73	1.22	45.26	21.29	16.06
5233-8	0.00	1.07	0.24	2.46	7.67	0.85	1.25	47.47	22.51	14.90
5233-9	0.00	0.94	0.58	5.37	9.06	0.68	1.42	46.70	20.26	13.95
5233-10	0.00	0.83	0.26	2.84	7.89	0.74	1.26	46.21	21.68	16.88
5233-11	0.00	1.06	0.19	1.78	7.43	0.69	1.16	49.30	21.79	15.07
5233-12	0.00	0.69	0.51	5.42	9.02	0.77	1.40	46.09	19.81	15.03
5233-13	0.00	0.65	0.04	0.11	5.49	0.46	1.25	51.21	22.32	16.82
5233-14	0.00	0.81	0.64	6.46	9.54	0.86	1.21	44.11	20.50	14.33
5233-15	0.00	0.88	0.24	2.79	8.16	0.72	1.40	47.47	21.50	15.35
5233-16	0.00	1.00	0.35	3.52	8.03	0.66	1.35	44.98	23.01	15.94
5233-17	0.00	0.86	0.78	7.89	10.63	1.01	1.37	42.11	20.58	13.17
5233-18	0.00	1.53	0.62	6.25	10.14	0.83	1.37	39.80	23.38	15.64
5233-19	0.00	1.29	0.27	2.43	8.46	1.19	1.72	45.19	23.78	13.60
5233-20	0.00	1.23	0.34	3.59	9.49	1.03	1.87	48.74	19.24	12.93
5233-21	0.00	0.82	0.23	1.97	7.27	0.77	1.26	49.20	22.11	14.91
5233-22	0.00	0.60	0.54	5.63	9.64	0.75	1.56	45.07	21.94	12.53
5233-24	0.00	0.77	0.54	6.08	9.67	0.84	1.27	42.47	21.15	15.74
Control	0.00	0.74	0.02	0.10	6.15	0.66	1.48	51.75	21.03	16.22

15

An increased percentage of C14 fatty acyl groups above control plant background levels is observed in all but one of the transgenic plants analyzed. The levels of C14 range from approximately 2.0 mole percent to 11.5 mole percent.

Single seed data from transformants 5233-5 and 5233-6 are presented in Figure 9. These results demonstrate C14 levels of greater than 20% are obtained in seeds expressing a camphor FatB thioesterase. Increases in 16:0 levels from approximately 6 mole % in seeds from non-transformed control plants up to approximately 15 mole % are obtained. To a lesser extent, increases in 12:0 fatty acyl groups are also observed.

At lower levels of C14, the C16 levels may be up to 2-3 times that of the C14 levels. At higher C14 levels, the C16 levels are equal to or less than the C14 levels. A graph of the C14 and C16 levels in these transgenic plant seeds is provided in Figure 11. Total saturated fatty acid contents of up to 40 mole % are detected in these seeds.

C. *C. palustris* Expression Construct

Analysis of pooled seeds from 3863-transformants reveals C14 levels of up to approximately 37 mole percent. Data from analysis of fatty acid compositions of single seeds from transformants 3863-10, 3863-7, 3863-4, 3863-8, 3863-2, and 3863-5 are presented in Figure 10. These data indicate C14 levels of greater than 40% are obtained by expression of *C. palustris* FatB2 thioesterase clone. C14 levels exceed C16 levels at a ratio of approximately 2:1 in most of the 3863 transformant seeds. However, when C14 levels are low (less than approximately 15%), C16 levels are generally higher than C14 levels. A graph of the C14 and C16 levels in the nutmeg, *C. palustris* and camphor TE transgenic plant seeds is provided in Figure 11.

D. Oleosin Promoter/C14 Thioesterase Constructs

Analysis (mole percent fatty acids) of pooled seed samples from *B. napus* transgenic plants expressing the *C. palustris* (3864) or the nutmeg (3857) C14 thioesterases is provided in Figure 12. As with napin promoter constructs, expression of nutmeg thioesterase results in increased production of C14 and C16 fatty acids at a ratio of approximately 2:1 C16/C14 fatty acids. With expression of *C. palustris* C14 thioesterase, C14 is generally produced in greater amounts than C16 as was observed with napin/*C. palustris* C14 thioesterase constructs. Generally, levels of C14 and C16 fatty acids obtained by expression of thioesterases under regulatory control of the

oleosin promoter are lower than the levels obtained by expression using the napin promoter.

E. C14 thioesterase and Medium-chain LPAAT Expressing Plants

Napin/*C. palustris* transformant 3863-6, seeds of which

5 comprise approximately 20 mole percent 14:0 and 13 mole percent 16:0, is crossed with a *B. napus* transformant comprising a coconut medium-chain preferring LPAAT expression construct, pCGN5511. (See WO 95/27791.) Fatty acyl composition analysis of segregating pooled seeds from the resulting F1 plants reveal
10 average levels of 10 mole percent 14:0 and 7 mole percent 16:0. Fatty acyl composition at the sn-2 position are determined for pooled segregating seed samples from the 3863-6 plants and the F1 plants resulting from the 5511 X 3863-6 cross.

For sn-2 analysis oil distilled from mature seeds is
15 subjected to a lipase digestion protocol modified from Brockerhoff et al. (*Meth. Enzymol.* (1975) 35:315-325)), to minimize acyl migration. This distinguishes acyl compositions of the sn-2 and sn-1+3 combined positions. The modifications are briefly as follows: pH is lowered to neutrality, reaction
20 time is shortened, samples are maintained at acidic pH thereafter, and digestion products are chromatographed on borate-impregnated TLC plates. The chromatographed products are then eluted and analyzed as fatty acid methyl esters as before. In this manner the percentage of fatty acids, such as
25 medium-chain C12 or C14 fatty acids or long-chain C22:1 fatty acids in the sn-2 position is determined. The modified procedure was verified using stereochemically defined structured TAGs and is conducted as follows.

Generally in the lipase procedure, only positive-
30 displacement pipetors are used as oil and organic solvents cannot be delivered reliably by negative-displacement pipetors. Additionally, care should be taken when evaporating solvents to bring the sample only barely to dryness. When C10 or shorter acyl groups are present avoid dryness altogether. Plasticware
35 or kitchen glassware that can contribute fatty acid contamination should be avoided. Glassware may be pre-rinsed with chloroform/methanol 2/1 (v/v) if necessary.

In 15-ml screw-cap (teflon liner) vial combine 2 ml 0.1M Tris-HCl, pH 7.0, 0.2 ml 2.2% w/v CaCl_2 , 0.5 ml 0.05% w/v bile

salts (Sigma), and 10 μ l (10 μ g if solid) oil or TAG sample. Sonicate briefly in a sonication bath to disperse at least some of the oil. The suspension should develop a cloudy appearance after a few minutes.

- 5 Prepare lipase dilution using an active suspension of lipase, such as *Rhizopus arrhizus* lipase (Sigma, L4384) and hold on ice (4°C). (Activity will be lost if suspension is frozen). Enzyme batches may be checked by testing various dilutions of the suspension with water in the overall
- 10 procedure, using oil containing unsaturated fatty acids and visualizing the extent of digestion by System 1 TLC (see below) with iodine staining. The correct dilution should result in approximately 50% digestion of the TAG. (Further digestion risks increasing attack on the MAG product.) Typically
- 15 dilution of the Sigma *Rhizopus arrhizus* lipase suspension with water to about 600,000 units/ml gives an appropriate concentration.

- Each reaction is run individually. Add 100 μ l of the water-diluted lipase to start the reaction, cap the vial, and
- 20 immediately start a continuous vortex mixing for 1.5 minutes. Make and break the vortex several times during this mixing so as to prevent stratification. A white ppt must form during the 1.5 min "incubation". The precipitate comprises calcium salts of released fatty acids, and is an indication that the reaction
- 25 is proceeding.

- At the end of the 1.5 min mixing incubation, stop the reaction by adding 0.5 ml 6M HCl and mixing briefly. Immediately add 2.6 ml chloroform/methanol 2/1 v/v, shake well and place in ice while the other lipase digestions are
- 30 performed. Note that the white ppt will now completely redissolve.

- Remove all the vials from ice, mix well once again, and spin briefly to sharpen the layers. The digestion products are in the lower layer. Using a Pasteur pipet remove the lower
- 35 layer to a new 15-ml vial. Re-extract the original digestion mixture with 1.6 ml straight chloroform, mix well, spin, and combine this lower layer with the previously removed one. The combined lower, organic layers are blown to near-dryness under

N₂ and just enough heat to prevent the samples from getting very cold.

The TLC plates for acyl migration are 500 μ m preparative Sil-G pre-loaded with boric acid and containing no fluorescent indicator. The pre-loading is carried out by ascending migration of 5% w/v boric acid in 1/1 v/v acetonitrile/methanol for at least 90 minutes. The plates are dried and stored at room temperature until ready for use. Heating "activation" may be necessary in damp climates.

Two solvent systems are suitable, both ascending the plates for exactly 1 hour even if the solvent doesn't reach the top of the plate, as longer runs result in reduced resolution due to the extreme volatility of the solvents.

System 1 - n-hexane/diethyl ether/acetic acid, 70/30/1 v/v

System 2 - Diethyl ether/acetic acid, 100/1 v/v

System 1 is used to evaluate and monitor the lipase reaction, as it allows recovery of TAG, DAG, fatty acid, and MAG. System 2 may be used for routine use and yields the best purity of the MAG product required for the sn-2 determination.

Prior to spotting the plates, score down the middle with a pencil so that two samples can be applied (left and right). (Sample chromatography is performed in the same direction as the borate loading.) Also remove 0.5 cm of layer from each side to eliminate edge effects, and draw a line 2 cm up from the bottom as a loading guide. Redissolve each dried sample in 100 μ l chloroform/methanol 2/1 (v/v) and apply along the loading line on the half-plate. Rinse the vial twice with 100 μ l chloroform/methanol 2/1 (v/v) each time and load over the top of the sample. Air-dry the loading area and run the solvent. Let plates air-dry in hood.

To ensure minimal acyl rearrangements for sn-1 and sn-3 analyses of the products, the procedure should be conducted without interruption from the start of the lipase reaction.

The TLC plates are visualized with Rhodamine spray, ~1% w/v Rhodamine 6G in acetone. The plates are sprayed until they are an overall medium-pink color, allowed to dry a few minutes, and viewed under UV light. Lipids fluoresce yellow on an

orange background. Desired zones are outlined in pencil. When using system 2, MAG zone is routinely 50-75% of the distance up the plat and the rest of the products are at the top. The MAG area may appear multi-zoned due to some chain-length
5 resolution, but should be outlined for excision as a single overall zone.

The zones are scraped onto clean paper and transferred to large screw-cap (teflon liner) test tubes. Add 10 ml chloroform/methanol 2/1 (v/v), shake, and let stand for at
10 least an hour. Filter through Whatman paper directly into 100-ml rotary evaporation flasks. Rinse the tubes twice through the filters with 5 ml chloroform/methanol 2/1 (v/v) each time. (The Rhodamine dye will co-elute with the lipids and will track with them through the procedure until the final
15 hexane extraction of fatty acid methyl esters (FAMES), when it will be left behind.) Rotary-evaporate at room temperature or up to 30°C, to reduce volume to about 100 µl. Transfer to 15-ml screw-cap vial, along with a couple of 100 µl chloroform/methanol 2/1 (v/v) rinses of the flask, and blow
20 down to near-dryness under N₂.

To the nearly dry samples add 2 ml freshly-prepared 5% (w/v) sulfuric acid in methanol. Relatively new methanol which has not had a chance to absorb much water should be used. Also add to the samples 1 ml of toluene containing desired internal
25 standard at 0.5 mg/ml TAG (e.g. tri-17:0 etc.). Incubate at 90°C for 2 hours, tightening the caps after the first 2 minutes and again after about 15 minutes. After the vials have cooled, add 2 ml 0.9% w/v NaCl and 0.5 ml n-hexane. Mix thoroughly, let stand a few minutess to separate layers, and sample the top
30 layer into the g.c. vial. Fatty acid composition is determined by analysis for fatty acid methyl esters (FAME) as described by Browse et al. (*Anal. Biochem.* (1986) 152:141-145).

The composition of the MAG zone is taken as the composition at *sn*-2 of the original oil or TAG sample. The
35 average composition at the primary (*sn*-1 and -3) positions is computed using the formula $(3\text{TAG}-\text{MAG})/2$ on the % of each acyl group.

The *sn*-2 analysis of T2 seed from 3863-6 reveals a 14:0 level of approximately 3 mole percent. Levels of 16:0 at the

sn-2 position were less than 1 mole percent. Analysis of *sn*-2 fatty acyl groups in F1 seeds from a 5511 X 3863-6 plant indicates 14:0 levels of approximately 9 mole percent. As with the 3863-6 plant seeds, the levels of 16:0 at the *sn*-2 position were less than 1 mole percent.

These data demonstrate that the expression of coconut medium-chain LPAAT in conjunction with expression of a plant C14 thioesterase provides for greater incorporation of myristate into the *sn*-2 position, effectively randomizing the distribution of 14:0, while the 16:0 distribution is unaffected. Thus, the combination of LPAAT and C14 thioesterase is especially desirable for overall increase in C14 fatty acids in transgenic plant seed oils.

The above results demonstrate the ability to obtain DNA sequences which encode thioesterase activities, which sequences may be expressed in plant seed cells for manipulation of seed oil fatty acid composition. In this manner production of significant levels of C14 fatty acids C14 may be obtained. The novel seed oils so produced may find uses in industry as whole oils, or can be fractionated using methods known in the industry to provide sources of the C14 fatty acids incorporated into the oil.

All publications and patent applications mentioned in this specification are indicative of the level of skill of those skilled in the art to which this invention pertains. All publications and patent applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications may be practiced within the scope of the appended claim.

What is claimed is:

1. A method of producing C14 fatty acids in plant seed triglycerides, wherein said method comprises:
 - 5 growing a plant having integrated into its genome a DNA construct, said construct comprising in the 5' to 3' direction of transcription, a promoter functional in a plant seed cell, a DNA sequence encoding a protein having preferential hydrolysis activity on C14:0 acyl-ACP substrates as compared to other
 - 10 medium-chain acyl-ACP substrates, and a transcription termination region functional in a plant cell.
2. The method of Claim 1 wherein said plant is an oilseed crop plant.
3. The method of Claim 2 wherein said oilseed crop plant
- 15 is a *Brassica* plant.
4. The method of Claim 1, wherein said protein is a plant acyl-ACP thioesterase.
5. The method of Claim 4 wherein said plant thioesterase encoding sequence is from *Cuphea*, nutmeg or camphor.
- 20 6. The method of Claim 4, wherein said plant acyl-ACP thioesterase has preferential activity on C14 acyl-ACP substrates.
7. The method of Claim 6, wherein said plant thioesterase encoding sequence is from *Cuphea palustris*.
- 25 8. The method of Claim 1, wherein said promoter is from a gene preferentially expressed in plant seed tissue.
9. The method of Claim 1, wherein said plant seed triglycerides comprise at least 5 mole percent C14 fatty acyl groups.
- 30 10. The method of Claim 1, wherein said plant seed triglycerides comprise at least 20 mole percent C14 fatty acyl groups.
11. The method of Claim 1, wherein said plant seed triglycerides comprise at least 40 mole percent C14 fatty acyl
- 35 groups.
12. The method of Claim 1, wherein said plant seed triglycerides further comprise increased 16:0 fatty acyl content.

13. The method of Claim 12, wherein the level of 14:0 fatty acyl groups is greater than the level of 16:0 fatty acyl groups.

14. The method of Claim 12, wherein the level of 14:0
5 fatty acyl groups is less than the level of 16:0 fatty acyl groups.

15. A plant seed comprising a minimum of 5.0 mole percent myristate in total fatty acids, wherein said myristate is incorporated into at least one position of a triglyceride
10 molecule and wherein wild-type seed of said plant contains less than 1.0 mole percent laurate in fatty acids.

16. The seed of Claim 15 comprising a minimum of about 20 mole percent myristate in fatty acids.

17. The seed of Claim 15 comprising a minimum of about 40
15 mole percent myristate in fatty acids.

18. Plant seed oil, wherein a minimum of 5.0 mole percent of the acyl groups of said oil are myristyl acyl groups, and wherein said oil is derived from a seed of Claim 15.

19. A *Brassica* seed comprising a minimum of 5.0 mole
20 percent myristate in total fatty acids.

20. Plant seed oil, wherein a minimum of 5.0 mole percent of the acyl groups of said oil are myristyl acyl groups, and wherein said oil is derived from a *Brassica* seed of Claim 19.

21. A DNA construct comprising an encoding sequence for a
25 plant acyl-ACP thioesterase having preferential activity on C14 acyl-ACP substrates as compared to other medium-chain acyl-ACP substrates.

22. A construct according to Claim 21 wherein said plant
30 is a *Cuphea* species.

23. A construct according to Claim 22 wherein said species is *Cuphea palustris*.

24. A construct according to Claim 23 wherein said thioesterase comprises the amino acid sequence shown in Figure 1.

25. A construct according to Claim 22 wherein said plant
35 is nutmeg.

26. A construct according to Claim 25 wherein said thioesterase comprises the amino acid sequence shown in Figure 2 or 3.

GCTCTAATAC GACTCACTAT AGGGAAGCT GGTACGCCTG CAGGTACCGG TCCGGAATTC 60
 CCGGGTCGAC CCAACGGTCC GCTGAGTTTG CTGGTTACCA TTTTCCCTGC GAACAAAC 118
 ATG GTG GCT GCC GCA GCA AGT GCT GCA TTC TTC TCC GTC GCA ACC CCG 166
 Met Val Ala Ala Ala Ser Ala Phe Phe Ser Val Ala Thr Pro 15
 1 5 10
 CGA ACA AAC ATT TCG CCA TCG AGC TTG AGC GTC CCC TTC AAG CCC AAA 214
 Arg Thr Asn Ile Ser Pro Ser Ser Leu Ser Val Pro Phe Lys Pro Lys 30
 20 25
 TCA AAC CAC AAT GGT GGC TTT CAG GTT AAG GCA AAC GCC AGT GCC CAT 262
 Ser Asn His Asn Gly Gly Phe Gln Val Lys Ala Asn Ala Ser Ala His 45
 35 40
 CCT AAG GCT AAC GGT TCT GCA GTA AGT CTA AAG TCT GGC AGC CTC GAG 310
 Pro Lys Ala Asn Gly Ser Ala Val Ser Leu Lys Ser Gly Ser Leu Glu 60
 50 55
 ACT CAG GAG GAC AAA ACT TCA TCG TCG TCC CCT CCT CGG ACT TTC 358
 Thr Gln Glu Asp Lys Thr Ser Ser Ser Pro Pro Pro Arg Thr Phe 70
 65 75 80

FIG.1A

ATT AAC CAG TTG CCC GTC TGG AGT ATG CTT CTG TCT GCA GTC ACG ACT 406
 ile Asn Gln Leu Pro Val Trp Ser Met Leu Leu Ser Ala Val Thr Thr
 85 90 95

 GTC TTC GGG GTG GCT GAG AAG CAG TGG CCA ATG CTT GAC CGG AAA TCT 454
 val phe Gly Val Ala Glu Lys Gln Trp Pro Met Leu Asp Arg Lys Ser
 100 105 110

 AAG AGG CCC GAC ATG CTT GTG GAA CCG CTT GGG GTT GAC AGG ATT GTT 502
 Lys Arg Pro Asp Met Leu Val Glu Pro Leu Gly Val Asp Arg ile Val
 115 120 125

 TAT GAT GGG GTT AGT TTC AGA CAG AGT TTT TCG ATT AGA TCT TAC GAA 550
 Tyr Asp Gly Val Ser phe Arg Gln Ser phe Ser ile Arg Ser Tyr Glu
 130 135 140

 ATA GGC GCT GAT CGA ACA GCC TCG ATA GAG ACC CTG ATG AAC ATG TTC 598
 ile Gly Ala Asp Arg Thr Ala Ser ile Glu Thr Leu Met Asn Met phe
 145 150 155 160

 CAG GAA ACA TCT CTT AAT CAT TGT AAG ATT ATC GGT CTT CTC AAT GAC 646
 Gln Glu Thr Ser Leu Asn His Cys Lys ile ile Gly Leu Leu Asn Asp
 165 170 175

FIG.1B

694
 GGC TTT GGT CGA ACT CCT GAG ATG TGT AAG AGG GAC CTC ATT TGG GTG
 Gly Phe Gly Arg Thr Pro Glu Met Cys Lys Arg Asp Leu Ile Trp Val
 180 185 190

742
 GTC ACG AAA ATG CAG ATC GAG GTG AAT CGC TAT CCT ACT TGG GGT GAT
 Val Thr Lys Met Gln Ile Glu Val Asn Arg Tyr Pro Thr Trp Gly Asp
 195 200 205

790
 ACT ATA GAG GTC AAT ACT TGG GTC TCA GCG TCG GGG AAA CAC GGT ATG
 Thr Ile Glu Val Asn Thr Trp Val Ser Ala Ser Gly Lys His Gly Met
 210 215 220

838
 GGT CGA GAT TGG CTG ATA AGT GAT TGC CAT ACA GGA GAA ATT CTT ATA
 Gly Arg Asp Trp Leu Ile Ser Asp Cys His Thr Gly Glu Ile Leu Ile
 225 230 235 240

886
 AGA GCA ACG AGC GTG TGG GCT ATG ATG AAT CAA AAG ACG AGA AGA TTG
 Arg Ala Thr Ser Val Trp Ala Met Met Asn Gln Lys Thr Arg Arg Leu
 245 250 255

934
 TCG AAA ATT CCA TAT GAG GTT CGA CAG GAG ATA GAG CCT CAG TTT GTG
 Ser Lys Ile Pro Tyr Glu Val Arg Gln Glu Ile Glu Pro Gln Phe Val
 260 265 270

FIG.1C

GAC TCT GCT CCT GTC ATT GTA GAC GAT CGA AAA TTT CAC AAG CTT GAT 982
 Asp Ser Ala Pro Val Ile Val Asp Asp Arg Lys Phe His Lys Leu Asp
 275 280 285
 TTG AAG ACC GGT GAT TCC ATT TGC AAT GGT CTA ACT CCA AGG TGG ACT 1030
 Leu Lys Thr Gly Asp Ser Ile Cys Asn Gly Leu Thr Pro Arg Trp Thr
 290 295 300
 GAC TTG GAT GTC AAT CAG CAC GGT AAC AAT GTG AAA TAC ATC GGG TGG 1078
 Asp Leu Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly Trp
 305 310 315
 ATT CTC CAG AGT GTT CCC ACA GAA GAA GTT TTC GAG ACG CAG GAG CTA TGT 1126
 Ile Leu Gln Ser Val Pro Thr Thr Glu Val Phe Glu Thr Thr Gln Glu Leu Cys
 320 325 330
 GGC CTC ACC CTT GAG TAT AGG CGA GAA TGC GGA AGG GAC AGT GTG CTG 1174
 Gly Leu Thr Leu Glu Tyr Arg Arg Glu Cys Gly Arg Asp Ser Val Leu
 340 345 350
 GAG TCC GTG ACC GCT ATG GAT CCA TCA AAA GAG GGA GAC CGG TCT CTT 1222
 Glu Ser Val Thr Ala Met Asp Pro Ser Lys Glu Gly Asp Arg Ser Leu
 355 360 365

FIG.1D

TAC CAG CAC CTT CTC CGA CTC GAG GAC GGG GCT GAT ATC GTC AAG GGG 1270
Tyr Gln His Leu Leu Arg Leu Glu Asp Gly Ala Asp Ile Val Lys Gly
370 375 380

AGA ACC GAG TGG CCG CCG AAG AAT GCA GGA GCC AAG GGA GCA ATA TTA 1318
Arg Thr Glu Trp Arg Pro Lys Asn Ala Gly Ala Lys Gly Ala Ile Leu
385 390 395 400

ACC GGA AAG ACC TCA AAT GGA AAC TCT ATA TCT TAGAAGGAGG AAGGACCTT 1371
Thr Gly Lys Thr Ser Asn Gly Asn Ser Ile Ser
405 410

TCCGAGTTGT GTGTTTATTT GCTTTGCTTT GATTCACCTCC ATTGTATAAT AATACTACGG 1431

TCAGCCGTCT TTGTATTTC TAAGACAAAT AGCACAGTCA TTAAGTTAAA AAAAAAAAAA 1491

AAGGGCGGCC GCTCTAGAGG ATCCAAGCTT ACGTACGGGT GCATGCGACG TCATAGCTCT 1551

TCTATAGTGT CACCTAAATT CAATTCAC TG 1581

FIG.1E

48
 CCG GAT TGG AGC ATG CTT GCA GCA ATC ACA ACC ATC TTC TTG GCA
 Pro Asp Trp Ser Met 5
 1
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 96
 GCC GAG AAG CAG TGG ACG AAT CTT GAC TGG AAG CCC AGG AGG CCT GAC
 Ala Glu Lys Gln Trp Thr Asn Leu Asp 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 144
 ATG CTC GTC GAC TTT GAC CCT TTT AGT CTG GGG AGG TTC GTT CAG GAT
 Met Leu Val Asp Phe Asp Pro Phe Ser Leu Gly Arg Phe Val Gln Asp
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 192
 GGG TTG ATT TTC AGG CAG AAT TTC TCC ATC AGG TCT TAT GAG ATT GGC
 Gly Leu Ile Phe Arg Gln Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 240
 GCG GAT CGG ACG GCA TCC ATA GAG ACG TTA ATG AAT CAT CTA CAG GAA
 Ala Asp Arg Thr Ala Ser Ile Glu Thr Leu Met Asn His Leu Gln Glu
 65
 70
 75
 80
 85
 90
 95
 288
 ACG GCC CTA AAC CAT GTA AGG TGT ATA GGG CTC CTC GAT GAT GGT TTT
 Thr Ala Leu Asn His Val Arg Cys Ile Gly Leu Leu Asp Asp Gly Phe
 85
 90
 95

FIG. 2A

GGT TCG ACG CCT GAG ATG ACT AGG AGA GAT CTG ATA TGG GTG GTT ACA 336
 Gly Ser Thr Pro Glu Met Thr Arg Arg Asp Leu Ile Trp Val Val Thr
 100 105 110

AGG ATG CAG GTT CTG GTG GAT CGC TAT CCT TCC TGG GGG GAT GTC ATT 384
 Arg Met Gln Val Leu Val Asp Arg Tyr Pro Ser Trp Gly Asp Val Ile
 115 120 125

GAA GTA GAC TCC TGG GTT ACT CCA TCT GGA AAG AAT GGG ATG AAA CGT 432
 Glu Val Asp Ser Trp Val Thr Pro Ser Gly Lys Asn Gly Met Lys Arg
 130 135 140

GAA TGG TTT CTC CGT GAT TGC AAG ACA GGC GAA ATC CTG ACA CGA GCT 480
 Glu Trp Phe Leu Arg Asp Cys Lys Thr Gly Glu Ile Leu Thr Arg Ala
 145 150 155 160

ACC AGT GTT TGG GTG ATG ATG AAT AAA CGG ACA CGG AGG TTG TCC AAA 528
 Thr Ser Val Trp Val Met Met Asn Lys Arg Thr Arg Arg Leu Ser Lys
 165 170 175

ATC CCT GAA GAA GTT AGA GTC GAA ATA GAG CCT TAT TTT GTG GAG CAT 576
 Ile Pro Glu Glu Val Arg Val Glu Ile Glu Pro Tyr Phe Val Glu His
 180 185 190

FIG.2B

624	GGA GTC TTG GAT GAG GAC AGC AGA AAA CTA CCA AAG CTC AAT GAC AAC Gly Val Leu Asp Glu Asp Ser Arg Lys Leu Pro Lys Leu Asn Asp Asn 195 200 205
672	ACT GCA AAT TAC ATC AGA AGA GGC CTA GCT CCT CGG TGG AGT GAT TTA Thr Ala Asn Tyr Ile Arg Arg Gly Leu Ala Pro Arg Trp Ser Asp Leu 210 215 220
720	GAT GTC AAT CAG CAT GTG AAC AAT AAT GTC AAA TAC ATT GGC TGG ATT CTT Asp Val Asn Gln His Val Asn Asn Val Lys Tyr Ile Gly Trp Ile Leu 225 230 235 240
768	GAG AGC GTG CCA TCT TCA CTG TTG GAG AGT CAT GAG CTG TAT GGG ATG Glu Ser Val Pro Ser Ser Leu Leu Glu Ser His Glu Leu Tyr Gly Met 245 250 255
816	ACA CTT GAG TAT AGG AAG GAG TGT CGA AAG GAC GGT TTG CTG CAA TCC Thr Leu Glu Tyr Arg Lys Glu Cys Gly Lys Asp Gly Leu Leu Gln Ser 260 265 270
864	CTG ACT GCT GTT GCC AGT GAT TAT GGG GGT GGA TCC CTT GAA GCT GGC Leu Thr Ala Val Ala Ser Asp Tyr Gly Gly Gly Ser Leu Glu Ala Gly 275 280 285

FIG.2C

GTT GAG TGT GAC CAC CTT CTT CGC CTT GAA GAT GGG AGT GAG ATT ATG 912
Val Glu Cys Asp His Leu Leu Arg Arg Glu Asp Gly Ser Glu Ile Met
290 295 300

AGG GGA AAG ACG GAA TGG AGG CCC AAG CGT GCC GCC AAC ACT ACC TAC 960
Arg Gly Lys Thr Glu Trp Arg Pro Lys Arg Ala Ala Asn Thr Thr Tyr
305 310 315 320

TTT GGA AGC GTT GAT GAT ATT CCT CCC CAC CCA ATA TAT ATA TAT ATA 1008
Phe Gly Ser Val Asp Asp Ile Pro Pro His Pro Ile Tyr Ile Tyr Ile
325 330 335

TAT ATA TAT ATA TAT ATA TAT TGG GTG GGG AGC AGC TGC AGC 1056
Tyr Ile Tyr Ile Tyr Ile Tyr Ile Tyr Trp Val Gly Ser Ser Cys Ser
340 345 350

GGC AGC AGC ACG ACA ATG TCG AGG ACA CGA TGACCATCAG TATGTTTCGT 1106
Gly Ser Ser Thr Thr Met Ser Arg Thr Arg
355 360

GCGGTATTTA GCAATTCGGT ATGTAGAATC CTGCGTGTAC TGGCAGATAA TTTTGTGATT 1166

TGTTCTTTTC GTTTACGAGG GGAACCCGTC TAATTAGTTC AACTGTATTT TCTGTTTCTT 1226

FIG.2D

CCCTTAAGTGT TTCAACACCC CTCTCTCTCT CGCGCGGCGG CGTGGGCTCA CATTTTCCAT 1286
TCCTTTCTTT TTATATCTAG TTGTACGAGT GGGAGTTTCAT TTGCACATAA TTGTTGAAAA 1346
ATCTCGTTGC TTGG 1360

FIG.2E

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GGAGAGCCGC CTCTTCAGCC CACCACCACC TCTAAAACAA CAGGCCCAA ACTCCCTCCT 60
TTCTCTGTCC CTTTCCGGTG CTCCCCCTC TATTTAGAC CTCCTCCTTT ATATTCCCA 120
ACGTAGAATA ATACCAAAC CCTAAACCGA GAAGAAGATA AAAGAAAGAG GAGAGAGAAA 180
CAGAAAGAGA TAGAGAGAGA AAAAAATCG GTCTTCTCTC TCTTCTCTG TCGCTCGAA 240
GGAGCGGCGG TGAAATTGG TCATTGCTA TGAGAAATAT TCCTTCTGTG ATGCTTGATT 300
TCTAATTAA CGAGTCTGTA TCGTAATTT CTCATC ATG GTT GCC ACA TCT GCT 354
Met Val Ala Thr Ser Ala
1 5
GCC TCC GCT TTC TTC CCG GTT GCC TCT CCG TCT CCA GTG AAG CCT TCG 402
Ala Ser Ala Phe Phe Pro Val Ala Ser Pro Ser Pro Val Lys Pro Ser
10 15 20
ATG ATG CTC GGT GGT GGA GGA GGT TCG GAT AAT CTC GAC GCC CGT GGG 450
Met Met Leu Gly Gly Gly Gly Ser Asp Asn Leu Asp Ala Arg Gly
25 30 35
ATC AAA TCC CGC CCT GCC TCC TCT GGT GCC CTT CAA GTA AAG GCC AAT 498
Ile Lys Ser Arg Pro Ala Ser Ser Gly Gly Leu Gln Val Lys Ala Asn
40 45 50

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FIG.3A

546 GCT CAT ACT GTT CCC AAG ATC AAT GGT AAC AAG GCG GGC CTT TTG ACG
 Ala His Thr Val Pro Lys 60 Ile Asn Gly Asn Lys Ala Gly Leu Thr 70
 55

594 CCT ATG GAG AGC ACT AAG GAC GAG GAC ATC GTG GCT GCC CCA ACG GTT
 Pro Met Glu Ser Thr 75 Lys Asp Glu Asp Ile Val Ala Ala Pro Thr Val
 85

642 GCT CCT AAG AGG ACT TTC ATC AAC CAG CTG CCG GAT TGG AGC ATG CTT
 Ala Pro Lys Arg Thr Phe 90 Ile Asn Gln Leu Pro Asp Trp Ser Met Leu
 95

690 CTT GCA GCA ATC ACA ACC ATC TTC TTG GCA GCC GAG AAG CAG TGG ACG
 Leu Ala Ala Ile Thr Thr 105 Phe Leu Ala Ala Glu Lys Gln Trp Thr
 110

738 AAT CTT GAC TGG AAG CCC AGG AGG CCT GAC ATG CTC GTC GAC TTT GAC
 Asn Leu Asp Trp Lys Pro Arg Arg Pro Asp Met Leu Val Asp Phe Asp
 120 125 130

786 CCT TTT AGT CTG GGG AGG TTC GTT CAG GAT GGG TTG ATT TTC AGG CAG
 Pro Phe Ser Leu Glu Gly Arg Phe Val Gln Asp Gly Leu Ile Phe Arg Gln
 135 140 145 150

FIG. 3B

AAT TTC TCC ATC AGG TCT TAT GAG ATT GGC GCG GAT CCG ACG GCA TCC	834
Asn Phe Ser Ile Arg Ser Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser	155 160 165
ATA GAG ACG TTA ATG AAT CAT CTA CAG GAA ACG GCC CTA AAC CAT GTA	882
Ile Glu Thr Leu Met Asn His Leu Gln Glu Thr Ala Leu Asn His Val	170 175 180
AGG TGT ATA GGG CTC CTC GAT GAT GAT GGT TTT GGT TCG ACG CCT GAG ATG	930
Arg Cys Ile Gly Leu Leu Asp Asp Gly Phe Gly Ser Thr Pro Glu Met	185 190 195
ACT AGG AGA GAT CTG ATA TGG GTG GTT ACA AGG ATG CAG GTT CTG GTG	978
Thr Arg Arg Asp Leu Ile Trp Val Val Thr Arg Met Gln Val Leu Val	200 205 210
GAT CGC TAT CCT TCC TGG GGG GAT GTC ATG GAA GTA GAC GAC TCC TGG GTT	1026
Asp Arg Tyr Pro Ser Trp Gly Asp Val Ile Glu Val Asp Ser Trp Val	215 220 225 230
ACT CCA TCT GGA AAG AAT GGG ATG AAA CGT GAA TGG TTT CTC CGT GAT	1074
Thr Pro Ser Gly Lys Asn Gly Met Lys Arg Glu Trp Phe Leu Arg Asp	235 240 245
TGC AAG ACA GGC GAA ATC CTG ACA CGA GCT ACC AGT GTT TGG GTG ATG	1122
Cys Lys Thr Gly Glu Ile Leu Thr Arg Ala Thr Ser Val Trp Val Met	250 255 260

FIG.3C

ATG AAT AAA CGG ACA CGG AGG TTG TCC AAA ATC CCT GAA GAA GTT AGA	1170
Met Asn Lys Arg Thr Arg Arg Leu Ser Lys Ile Pro Glu Glu Val Arg	
GTC GAA ATA GAG CCT TAT TTT GTG GAG CAT GGA GTC TTG GAT GAG GAC	1218
Val Glu Ile Glu Pro Tyr Phe Val Glu His Gly Val Leu Asp Glu Asp	
280 285 290	
AGC AGA AAA CTA CCA AAG CTC AAT AAT GAC AAC ACT GCA AAT TAC ATC AGA	1266
Ser Arg Lys Lys Leu Pro Lys Leu Asn Asp Asn Thr Ala Asn Tyr Ile Arg	
295 300 305 310	
AGA GGC CTA GCT CCT CGG TGG AGT GAT TTA GAT GTC AAT CAG CAT GTG	1314
Arg Gly Leu Ala Pro Arg Trp Ser Asp Leu Asp Val Asn Gln His Val	
315 320 325	
AAC AAT GTC AAA TAC ATT GGC TGG AGT ATT CTT GAG AGC GTG CCA TCT TCA	1362
Asn Asn Val Lys Tyr Ile Gly Trp Ile Leu Glu Ser Val Pro Ser Ser	
330 335 340	
CTG TTG GAG AGT CAT GAG CTG TAT GGG ATG ACA CTT GAG TAT AGG AAG	1410
Leu Leu Glu Ser His Glu Leu Tyr Gly Met Thr Leu Glu Tyr Arg Lys	
345 350 355	
GAG TGT GGA AAG GAC GGT TTG CTG CAA TCC CTG ACT GCT GTT GCC AGT	1458
Glu Cys Gly Lys Asp Gly Leu Leu Ser Leu Thr Ala Val Ala Ser	
360 365 370	

FIG.3D

GAT TAT GGG GGT GGA TCC CTT GAA GCT GGC GTT GAG TGT GAC CAC CTT 1506
Asp Tyr Gly Gly Ser Leu Glu Ala Gly Val Glu Cys Asp His Leu 390
375 380 385 400 405

CTT CGC CTT GAA GAT GGG AGT GAG ATT ATG AGG GGA AAG ACG GAA TGG 1554
Leu Arg Leu Glu Asp Gly Ser Glu Ile Met Arg Gly Lys Thr Glu Trp 405
395 410 415 420 425

AGG CCC AAG CGT GCC GCC AAC ACT ACC TAC TTT GGA AGC GTT GAT GAT 1602
Arg Pro Lys Arg Ala Ala Asn Thr Thr Tyr Phe Gly Ser Val Asp Asp 420
410 415 420 425 430

ATT CCT CCA GCA AAT AAT GCA TAGCCAAAAT GTATATATAT ATATATATAT 1653
Ile Pro Pro Ala Asn Asn Ala 425

ATATATATAT ATATATATAT ATATATATAT ATTGGGTGGG GAGCAGCTGC AGCGGCAGCA 1713

GCACGACAAT GTCGAGGACA CGATGACCAT CAGTATGTTT CGTGCGGTAT TTAGCAATTC 1773

CGTATGTAGA ATCCTGCGTG TACTGGCAGA TAATTTTTCG ATTGTCTCTT TTCGTTTACG 1833

AGGGGAACCC GTGTAATTAG TTCAACTGTA TTTTCTGTTT CTTCCTTAAG TGTTTCAACA 1893

FIG. 3E

CCCCCTCTCTC TCTCGCGCGC GCGCGTGCGC TCACATTTC CATTCCTTTT CTTTTTATTC 1953

TAGTTGTACG AGTGGGAGTT CATTGCACT 1983

FIG.3F

T CTA GAG TGG AAG CCG AAG CCG AAT CCA CCC CAG TTG CTT GAT GAC CAT 49
 Leu Glu Trp Lys Pro Lys Pro Asn Pro Pro Gln Leu Leu Asp Asp His 15
 1 5 10

TTT GGG CCG CAT GGG TTA GTT TTC AGG CGC ACC TTT GCC ATC AGA TCG 97
 Phe Gly Pro His Gly Leu Val Phe Arg Arg Thr Phe Ala Ile Arg Ser 30
 20 25

TAT GAG GTG GGA CCT GAC CGC TCC ACA TCT ATA GTG GCT GTT ATG AAT 145
 Tyr Glu Val Gly Pro Asp Arg Ser Thr Ser Ile Val Ala Val Met Asn 45
 35 40

CAC TTG CAG GAG GCT GCA CTT AAT CAT GCG AAG AGT GTG GGA ATT CTA 193
 His Leu Gln Glu Ala Ala Leu Asn His Ala Lys Ser Val Gly Ile Leu 50
 55 60

GGA GAT GGA TTC GGT ACG ACG CTA GAG ATG AGT AAG AGA GAT CTG ATA 241
 Gly Asp Gly Phe Gly Thr Thr Leu Glu Met Ser Lys Arg Asp Leu Ile 80
 65 70 75

TGG GTT GTG AAA CGC ACG CAT GTT GCT GTG GAA CGG TAC CCT GCT TGG 289
 Trp Val val Lys Arg Thr His Val Ala Val Glu Arg Tyr Pro Ala Trp 95
 85 90

GGT GAT ACT GTT GAA GTA GAG TGC TGG GTT GGT GCA TCG GGA AAT AAT 337
 Gly Asp Thr Val Glu Val Glu Cys Trp Val Gly Ala Ser Gly Asn Asn 110
 100 105

FIG.4A

385 GGC AGG CGC CAT GAT TTC CTT GTC CGG GAC TGC AAA ACA GGC GAA ATT
 Gly Arg Arg His Asp Phe Leu Val Arg Asp Cys Lys Thr Gly Glu Ile
 115 120 125

 433 CTT ACA AGA TGT ACC AGT CTT TCG GTG ATG ATG AAT ACA AGG ACA AGG
 Leu Thr Arg Cys Thr Ser Leu Ser Val Met Asn Thr Arg Thr Arg
 130 135 140

 481 AGG TTG TCC AAA ATC CCT GAA GAA GAT AGA GGG GAG ATA GGG CCT GCA
 Arg Leu Ser Lys Ile Pro Glu Glu Val Arg Gly Glu Ile Gly Pro Ala
 145 150 155 160

 529 TTC ATT GAT AAT GTG GCT GTC AAA GAC GAG GAA ATT AAG AAA CCA CAG
 Phe Ile Asp Asn Val Ala Val Lys Asp Glu Glu Ile Lys Lys Pro Gln
 165 170 175

 577 AAG CTC AAT GAC AGC ACT ACT GCA GAT TAC ATC CAA GGA GGA TTG ACT CCT
 Lys Leu Asn Asp Ser Thr Ala Asp Tyr Ile Gln Gly Gly Leu Thr Pro
 180 185 190

 625 CGA TGG AAT GAT TTG GAT ATC AAT CAG CAC Gln His Val Asn Ile Lys Tyr
 Arg Trp Asn Asp Leu Asp Ile Asn Gln His Val Asn Asn Ile Lys Tyr
 195 200 205

 673 GTT GAC TGG ATT CTT GAG ACT GTC CCA GAC TCA ATC TTT GAG AGT CAT
 Val Asp Trp Ile Leu Glu Thr Val Pro Asp Ser Ile Phe Glu Ser His
 210 215 220

FIG. 4B

CAT ATT TCC AGC TTC ACT ATT GAA TAC AGG AGA GAG TGC ACG AGG GAT 721
 His Ile Ser Ser Phe Thr Ile Glu Tyr Arg Arg Glu Cys Thr Arg Asp 240
 225 230 235
 AGC GTG CTG CAG TCC CTG ACC ACT CTC TCC GGT GGC TCG TCG GAA GCT 769
 Ser Val Leu Gln Ser Leu Thr Thr Val Ser Gly Gly Ser Ser Glu Ala 255
 245 250
 GGG TTA GTG TGC GAG CAC TTG CTC CAG CTT GAA GGT GGG TCT GAG GTA 817
 Gly Leu Val Cys Glu His Leu Leu Gln Leu Glu Gly Ser Glu Val 270
 260 265
 TTG AGG GCA AAA ACA GAG TGG AGG CCT AAG CTT ACC GAT AGT TTC AGA 865
 Leu Arg Ala Lys Thr Glu Thr Arg Pro Lys Leu Thr Asp Ser Phe Arg 285
 275 280
 GGG ATT AGT GTG ATA CCC GCA GAA TCG AGT GTC TAACTAACGA AAGAAGCATC 918
 Gly Ile Ser Val Ile Pro Ala Glu Ser Ser Val 295
 290
 TGATGAAGTT TCTCCTGTGC TGTGTTCGT GAGGATGCTT TTTAGAAGCT GCAGTTTGCA 978
 TTGCTTGTGC AGAATCATGG CCTGTGGTTT TAGATATATA TTCAAAAATTG TCCTATAGTC 1038
 AAGAAACTTA ATATCAGAAA AATAACTCAA TGAGTCAAGG TTATCGAAGT AGTCATGTAA 1098
 GCTTTGAAAT ATGTTGTGTA TTCCTCGGCT TTATGTAATC TGTAAAGCTCT TTCTCTTGC 1157

FIG.4C

48 GAA TTC GGC ACG AGG AGG GGC TCC GGT GCT TTG CAG GTG AAG GCA AGT TCC
 Glu Phe Gly Thr Arg 5 Ser Gly Ala Leu Gln Val Lys Ala Ser Ser 15

 96 CAA GCT CCA CCA AAG CTC AAT GGT TCC AAT GTG GGT TTG GTT AAA TCT
 Gln Ala Pro Pro Lys Leu Asn Gly Ser Asn Val Gly Leu Val Lys Ser 30
 20

 144 AGC CAA ATT GTG AAG AAG GGT GAT GAC ACC ACA TCT CCT CCT GCA AGA
 Ser Gln Ile Val Lys Lys Gly Asp 40 Thr Ser 45
 35

 192 ACT TTC ATC AAC CAA TTG CCT GAT TGG AGC ATG CTT CTT GCT GCT ATC
 Thr Phe Ile Asn Gln Leu Pro Asp 55 Met Leu Ala Ala Ile 60
 50

 240 ACA ACC CTG TTC TTG GCT GCA GAG AAG CAG TGG ATG ATG CTT GAT TGG
 Thr Thr Leu Phe Leu Ala Ala Glu Lys Gln Trp Met Met Leu Asp Trp 80
 65 70 75

 288 AAA CCC AAA AGG CCT GAC ATG CTT GTT GAT CCA TTT GGT CTT GGA AGG
 Lys Pro Lys Arg Pro Asp Met Leu Val Asp Pro Phe Gly Leu Gly Arg 95
 85 90

 336 TTT GTT CAG GAT GGT CTT GTT TTC CGC AAC AAC TTT TCA ATT CGA TCA
 Phe val Gln Asp Gly Leu val Phe Arg Asn Asn Phe Ser Ile Arg Ser 110
 100 105

FIG. 5A

384 TAT GAA ATA GGG GCT GAT CGA ACG GCT TCT ATA GAA ACG TTA ATG AAT
 Tyr Glu Ile Gly Ala Asp Arg Thr Ala Ser Ile Glu Thr Leu Met Asn
 115 120 125
 432 CAT CTG CAG GAA ACA GCT CTT AAT CAT GTG AAG TCT GTT GGG CTT CTT
 His Leu Gln Glu Thr Ala Leu Asn His Val Lys Ser Val Gly Leu Leu
 130 135 140
 480 GAG GAT GGC CTA GGT TCG ACT CGA GAG ATG TCC TTG AGG AAC CTG ATA
 Glu Asp Gly Leu Gly Ser Thr Arg Glu Met Ser Leu Arg Asn Leu Ile
 145 150 155 160
 528 TGG GTT GTC ACT AAA ATG CAG GTT GCG GTT GAT CGC TAT CCA ACT TGG
 Trp Val Val Thr Lys Met Gln Val Ala Val Asp Arg Tyr Pro Thr Trp
 165 170 175
 576 GGA GAT GAA GTT CAG GTA TCC TCT TGG GCT ACT GCA ATT GGA AAG AAT
 Gly Asp Glu Val Gln Val Ser Ser Trp Ala Thr Ala Ile Gly Lys Asn
 180 185 190
 624 GGA ATG CGT CGC GAA TGG ATA GTC ACT GAT TTT AGA ACT GGT GAA ACT
 Gly Met Arg Arg Glu Trp Ile Val Thr Asp Phe Arg Thr Gly Glu Thr
 195 200 205
 672 CTA TTA AGA GCC ACC AGT GTT TGG GTG ATG ATG AAT AAA CTG ACG AGG
 Leu Leu Arg Ala Thr Ser Val Trp Val Met Met Asn Lys Leu Thr Arg
 210 215 220

FIG. 5B

720 AGG ATA TCC AAA ATC CCA GAA GAG GTT TGG CAC GAA ATA GGC CCC TCT
 Arg Ile Ser Lys Ile Pro Glu Glu Val Trp His Glu Ile Gly Pro Ser 240
 225
 768 TTC ATT GAT GCT CCT CCT CTT CCC ACC GTG GAA GAT GAT GGT AGA AAG
 Phe Ile Asp Ala Pro Pro Leu Pro Thr Val Glu Asp Asp Gly Arg Lys 255
 245
 816 CTG ACA AGG TTT GAT GAA AGT TCT GCA GAC TTT ATC CGC NCT GGT TTA
 Leu Thr Arg Phe Asp Glu Ser Ser Ala Asp Phe Ile Arg Xxx Gly Leu 270
 260
 864 ACT CCT AGG TGG AGT GAT TTG GAC ATC AAC CAG CAT GTC AAC AAT GTG
 Thr Pro Arg Trp Ser Asp Leu Asp Ile Asn Gln His Val Asn Asn Val 285
 275
 912 AAG TAC ATT GGC TGG CTC CTT GAG AGT GCT CCG CCG GAG ATC CAC GAG
 Lys Tyr Ile Gly Trp Leu Leu Leu Ser Ala Pro Pro Glu Ile His Glu 300
 290
 960 AGT CAC GAG ATA GCG TCT CTG ACT CTG GAG TAC AGG AGG GAG TGT GGA
 Ser His Glu Ile Ala Ser Leu Thr Thr Leu Glu Tyr Arg Arg Glu Cys Gly 320
 305
 1008 AGG GAC AGC GTG CTG AAC TCC GCG ACC AAG GTC TCT GAC TCC TCT CAA
 Arg Asp Ser Val Leu Asn Ser Ala Thr Lys Val Ser Asp Ser Ser Gln 335
 325

FIG. 5C

23/37

CTG GGA AAG TCT GCT GTG GAG TGT AAC CAC TTG GTT CGT CTC CAG AAT 1056
Leu Gly Lys Ser Ala Val Glu Cys Asn His Leu Val Arg Leu Gln Asn 350
340

GGT GGG GAG ATT GTG AAG GGA AGG ACT GTG TGG AGG CCC AAA CGT CCT 1104
Gly Gly Glu Ile Val Lys Gly Arg Thr Val Trp Arg Pro Lys Arg Pro 365
355

CTT TAC AAT GAT GGT GCT GTT GTG GAC GTG NAA GCT AAA ACC TCT 1149
Leu Tyr Asn Asp Gly Ala Val Val Asp Val Xxx Ala Lys Thr Ser 380
370

TAAGTCTTAT AGTCCAAGTG AGGAGGAGTT CTATGTATCA GGAAGTTGCT AGGATTCTCA 1209

ATCGCATGTG TCCATTTCIT GTGTGGAATA CTGCTCGTGT TTCTAGACTC GCTATAATGT 1269

TGTTCITTTTA TATATATATA TATATATATA TCTCTCTCTT CCCCCCACCT CTCTCTCTCT 1329

CTCTATATAT ATATATGTTT TATGTAAGTT TTCCCCCTTAG TTTCCTTTCC TAAGTAATGC 1389

CATTGTAAAT TACTTCAAAA AAAAAAAAAA AAAAAAACT CGAG 1433

FIG. 5D

GGCAGAGAA ACAATGGTGGC TGCCGCAGCA AGTCTGCAAT TCTTCTCCGT TCCAACCCCG 60
GGAATCTCCC CTAACCCCG GAAGTTCGGT AATGGTGGCT TTCAGGTAA GGCAACGCC 120
AATGCCCATC CTAGTCTAAA GTCTGGCAGC CTCGAGACTG AAGATGACAC TTCATCGTCG 180
TCCCTCCTC CTCGGACTTT CATTAACCAG TTGCCCGACT GGAGTAIGCT TCTGTCCGCA 240
ATCAGACTA TCTTCGGGGC AGCTGAGAAG CAGTGGATGA TGCTTGATAG GAAATCTAAG 300
NAGACCCGAC ATGCTCATGG CAACCGTTTG GGGTTGACAG TATTGTTTTCAG GATGGGGTTT 360
TTTTCAGACA GAGTTTTTCG ATTAGATCTT ACGAAATAGG CGCTGATCGA ACAACCTCAA 420
TAGAGACGCT GATGAACATG TTCCAGGAAA CGTCTTTGAA TCATTGTAAG AGTAACGGTC 480
TTCTCAATGA CGGCTTTGGT CGCACTCCCTG AGATGTGTAA GAAGGGCCTC ATTGGGTGG 540
TTACGAAAT GCAGGTCGAG GTGAATCGCT ATCCTATTG GSGTGATTCT ATCGAAGTCA 600
ATACTTGGGT CTCCGAGTCG GGNAAAANC GGTATGGGTC GTGATTGGCT GATAAGTGAT 660

FIG. 6A

TGCAGTACAG GAGNAAATTC TTGTAAGAGC AACGAGCGTG TGGGCTATGA TGAATCAAAA 720
GACGAGAAGA TTGTCAAAT TTCCATTGA GGTTCGACAA GAGATAGCGC CTAATTTTGT 780
CGACTCTGTT CCTGTCAATG AAGACGATCG AAAATTACAC AAGCTTGATG TGAAGACGGG 840
TGAATCCATT CACAATGGTC TAACTCCAAG GTGGAATGAC TTGGATGTCA ATCAGCACGT 900
TAACAATGTG AAATACATG GGTGGATTCT CAAGAGTGTT CCAACACAGATG TTTTGGGGC 960
CCAGGAGCTA TGTGGA 976

FIG.6B

GGCGCGCCGG TACCTCTAGA CCTGGCGATT CAACGTGGTC GGATCATGAC GCTTCCAGAA 60
AACATCGAGC AAGCTCTCAA AGCTGACCTC TTTCGGATCG TACTGAACCC GAACAATCTC 120
GTTATGTCCC GTCGTCTCCG AACAGACATC CTCGTAGCTC GGATTATCGA CGAATCCAATG 180
GCTATACCCA ACCTCCGTCT TCGTCACGCC TGGAACCCCTC TGGTACGCCA ATTCCGCTCC 240
CCAGAAGCAA CCGGCGCCGA ATTGGCGGAA TTGCTGACCT GGAGACGGAA CATCGTCGTC 300
GGGTCCTTGC GCGATTGCGG CGGAAGCCGG GTCCGGTTGG GGACGAGACC CGAATCCGAG 360
CCTGGTGAAG AGGTTGTCA TCGGAGATTT ATAGACGGAG ATGGATCGAG CCGTTTGGG 420
GAAAGGGGAA GTGGGTTGG CTCTTTGG TAGAGAGAGT GCAGCTTGG AGAGAGACTG 480
GAGAGGTTA GAGAGAGACG CCGCGGATAT TACCGGAGGA GAGCGACGA GAGATAGCAT 540
TATCGAAGG GAGGAGAAA GAGTGACGTG GAGAAATAAG AAACCGTTAA GAGTCGGATA 600

FIG. 7A

TTTATCATAT TAAAAGCCCA ATGGGCCTGA ACCATTATA ACAAGACAGA TAAATGGGCC 660
GTGTGTTAAG TTAACAGAGT GTTAACGTTT GGTTCAAAT GCCAACGCCA TAGGAACAAA 720
ACAAACGTGT CCTCAAGTAA ACCCCTGCCG TTACACCTC AATGGCTGCA TGGTGAAGCC 780
ATTAACACGT GCGGTAGGAT GCATGACGAC GCCATTGACA CCTGACTCTC TTCCCTTCTC 840
TTCATATATC TCTAATCAAT TCAACTACTC ATTGTCATAG CTATTCGGAA AATACATACA 900
CATCCTTTTC TCTTCGATCT CTCICAATTC ACAAGAAGCA AAGTCGACGG ATCCCTGCAG 960
TAAATTACGC CATGACTATT TTCATAGTCC AATAAGGCTG ATGTCGGGAG TCCAGTTTAT 1020
GAGCAATAAG GTGTTTAGAA TTIGATCAAT GTTTATAATA AAAGGGGAA GATGATATCA 1080
CAGTCCTTTG TTCTTTTGG CTTTGTGTTAA ATTTGTGTGT TTCTATTGT AAACCTCCTG 1140
TATATGTGT ACTTCTTTCC CTTTTTAAGT GGTATCGTCT ATATGGTAA ACGTTATGTT 1200

FIG. 7B

TGGTCTTTCC TTTTCTCTGT TTAGGATAAA AAGACTGCAT GTTTTATCTT TAGTTATATT 1260
ATGTTGAGTA AATGAACCTT CATAGATCTG GTTCCGTAGA GTAGACTAGC AGCCGAGCTG 1320
AGCTGAACTG AACAGCTGGC AATGTGAACA CTGGATGCAA GATCAGATGT GAAGATCTCT 1380
AATATGGTGG TGGGATTGAA CATATCGTGT CTATATTTTT GTTGGCATTA AGCTCTTAAC 1440
ATAGATATAA CTGATGCAGT CATTTGGTTCA TACACATATA TAGTAAGGAA TTACAATGGC 1500
AACCCTAACT TCAAAAACAG TAGGCCACCT GAATGCCCTT ATCGAATAAG AGTTTGTTC 1560
CCCCCACTC ATGGGATGTA ATACATGGGA TTTGGGAGTT TGAATGAACG TTGAGACATG 1620
GCAGAACCTC TAGAGGTACC GCGCGGC 1647

FIG. 7C

SAMPLE	% 8:0	% 10:0	% 12:0	% 14:0	% 16:0	% 16:1	% 18:0	% 18:1	% 18:2	% 18:3	% 20:0	% 20:1	% 20:2	% 22:0	% 22:1	% 22:2
3854-3	0.00	1.84	0.03	0.07	4.54	0.21	2.62	69.78	17.22	1.34	0.78	1.16	0.04	0.38	0.00	0.00
3854-3	0.00	1.53	0.12	7.63	21.94	0.25	7.00	44.67	12.99	1.00	1.65	0.65	0.01	0.57	0.00	0.00
3854-3	0.00	0.15	0.27	16.40	31.31	0.45	7.02	25.70	15.12	0.91	1.78	0.36	0.00	0.51	0.00	0.00
3854-3	0.00	0.80	0.22	14.53	29.02	0.37	7.05	29.67	14.58	0.96	1.81	0.45	0.01	0.54	0.00	0.00
3854-3	0.00	1.46	0.30	18.86	32.21	0.31	7.50	22.53	12.67	0.85	2.26	0.33	0.01	0.71	0.00	0.00
3854-3	0.00	3.94	0.28	15.46	28.46	0.49	7.09	26.38	14.72	0.92	1.58	0.29	0.00	0.38	0.00	0.01
3854-3	0.00	2.15	0.24	19.46	33.03	0.20	6.19	23.09	11.66	0.93	2.06	0.31	0.00	0.68	0.00	0.00
3854-3	0.00	3.81	0.12	16.79	32.73	0.35	7.69	23.07	10.83	0.96	2.54	0.26	0.00	0.86	0.00	0.00
3854-3	0.00	6.40	0.38	20.90	30.38	0.41	6.27	21.28	10.61	0.90	1.79	0.22	0.02	0.40	0.01	0.00
3854-3	0.00	6.28	0.45	23.89	37.77	0.37	9.59	13.52	4.02	0.23	2.47	0.60	0.00	0.81	0.00	0.00
3854-3	0.00	1.04	0.04	0.09	4.49	0.11	2.31	69.29	18.94	1.42	0.75	1.19	0.02	0.31	0.00	0.00
3854-3	0.00	3.04	0.18	19.35	32.37	0.31	7.35	22.76	10.24	0.98	2.35	0.29	0.00	0.76	0.01	0.00
3854-11	0.00	1.39	0.33	17.95	30.29	0.66	6.77	23.35	15.37	1.03	1.87	0.35	0.01	0.62	0.00	0.00
3854-11	0.00	1.93	0.36	21.31	31.37	0.34	6.09	22.92	12.38	1.05	1.96	0.06	0.02	0.20	0.01	0.00
3854-11	0.00	1.22	0.27	18.75	31.33	0.50	6.91	25.50	13.08	0.89	1.12	0.31	0.01	0.11	0.01	0.01
3854-11	0.00	1.53	0.23	17.30	33.28	0.56	1.25	29.63	14.07	0.41	0.90	0.30	0.01	0.49	0.00	0.04
3854-11	0.00	0.50	0.03	0.04	3.93	0.07	2.92	76.55	12.30	0.99	0.95	1.27	0.02	0.42	0.01	0.00
3854-11	0.00	0.91	0.35	16.96	30.43	0.45	7.67	25.02	15.14	0.85	1.57	0.31	0.00	0.34	0.00	0.00
3854-11	0.00	1.44	0.38	23.03	33.37	0.45	7.07	19.31	11.50	0.98	1.73	0.23	0.00	0.52	0.01	0.00
3854-11	0.00	2.17	0.30	18.27	32.78	0.43	7.17	24.74	10.03	0.82	2.30	0.29	0.01	0.70	0.00	0.00
3854-11	0.00	1.73	0.29	21.83	32.82	0.30	7.41	20.85	11.18	0.71	2.07	0.19	0.00	0.61	0.00	0.00
3854-11	0.00	1.50	0.42	23.00	32.88	0.42	6.86	17.89	13.69	0.86	1.74	0.23	0.00	0.50	0.00	0.00
3854-11	0.00	2.16	0.34	21.37	36.03	0.27	8.12	19.29	8.56	0.60	2.25	0.25	0.00	0.75	0.01	0.00
3854-11	0.00	2.71	0.32	20.56	33.43	0.79	7.70	20.91	10.42	0.88	1.66	0.17	0.01	0.44	0.00	0.00

Figure 8

SAMPLE	% 8:0	% 10:0	% 12:0	% 14:0	% 16:0	% 16:1	% 18:0	% 18:1	% 18:2	% 18:3	% 20:0	% 20:1	% 20:2	% 22:0	% 22:1	% 22:2
5233-5	0.00	0.00	1.01	10.88	12.07	0.45	1.63	45.12	15.93	12.05	0.22	0.66	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	0.62	6.78	10.89	0.42	1.52	48.26	16.45	14.04	0.31	0.71	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	0.32	5.22	11.15	0.62	1.33	46.32	19.06	14.81	0.38	0.79	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	1.10	11.92	13.11	0.48	1.17	41.16	18.63	12.06	0.08	0.22	0.06	0.00	0.00	0.00
5233-5	0.00	0.00	0.47	6.39	12.06	0.49	1.55	44.78	20.34	13.11	0.16	0.62	0.00	0.05	0.00	0.00
5233-5	0.00	0.00	1.60	14.96	13.99	0.46	1.26	38.28	16.52	12.19	0.09	0.61	0.00	0.00	0.05	0.00
5233-5	0.00	0.00	1.74	15.07	12.96	0.46	1.48	40.24	15.80	11.54	0.08	0.54	0.00	0.00	0.03	0.03
5233-5	0.00	0.00	1.21	12.56	12.78	0.48	1.48	43.93	14.62	11.86	0.33	0.76	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	0.97	11.85	14.12	0.56	1.23	41.07	17.69	11.87	0.08	0.49	0.00	0.04	0.00	0.04
5233-5	0.00	0.00	0.83	8.97	12.39	0.42	1.58	48.28	16.85	9.56	0.34	0.69	0.04	0.06	0.00	0.00
5233-5	0.00	0.00	0.93	10.31	12.40	0.48	1.79	47.27	14.61	11.15	0.33	0.67	0.00	0.00	0.04	0.00
5233-5	1.84	0.00	0.08	0.13	7.23	0.17	1.62	53.76	19.19	14.81	0.31	0.85	0.00	0.00	0.00	0.00
5233-5	0.00	0.00	1.08	11.33	11.69	0.41	1.37	48.20	13.69	11.39	0.25	0.57	0.00	0.04	0.00	0.00
5233-5	0.00	0.00	0.92	11.49	13.95	0.63	1.15	39.54	18.18	13.09	0.24	0.68	0.08	0.01	0.00	0.03
5233-5	0.00	0.00	0.63	8.78	12.57	0.33	1.10	43.92	18.31	13.42	0.19	0.67	0.07	0.00	0.00	0.00
5233-5	0.00	0.00	1.80	17.17	14.47	0.54	1.23	38.34	15.29	10.44	0.14	0.56	0.00	0.00	0.00	0.01
5233-5	0.00	0.00	1.95	17.01	14.57	0.70	1.29	35.66	17.51	10.43	0.21	0.64	0.02	0.00	0.00	0.00
5233-5	0.00	0.00	0.87	11.22	13.23	0.40	1.29	40.45	18.98	12.75	0.16	0.54	0.00	0.09	0.02	0.00
5233-5	0.00	0.00	1.03	11.39	12.29	0.41	1.70	44.98	14.84	11.99	0.43	0.83	0.02	0.03	0.02	0.03
5233-5	0.00	0.00	0.76	8.93	13.19	0.20	1.26	41.27	19.80	14.12	0.07	0.34	0.00	0.00	0.08	0.00
5233-5	0.00	0.00	1.10	11.90	11.95	0.46	1.68	45.86	13.59	12.37	0.32	0.72	0.00	0.04	0.00	0.00
5233-5	0.00	0.00	1.05	10.72	12.43	0.44	1.49	43.90	15.96	13.12	0.15	0.70	0.00	0.05	0.00	0.00
5233-5	0.00	0.00	1.04	11.64	12.34	0.44	1.66	45.20	14.22	12.35	0.31	0.69	0.04	0.07	0.00	0.00
5233-5	0.00	0.37	0.45	4.76	11.20	0.12	0.94	45.76	21.36	14.10	0.09	0.83	0.00	0.02	0.00	0.00
5233-5	0.00	0.00	1.51	15.42	14.10	0.53	1.48	39.41	14.68	12.21	0.08	0.58	0.00	0.00	0.02	0.00

Figure 9A

SAMPLE	% 8:0	% 10:0	% 12:0	% 14:0	% 16:0	% 16:1	% 18:0	% 18:1	% 18:2	% 18:3	% 20:0	% 20:1	% 20:2	% 22:0	% 22:1	% 22:2
5233-6	0.00	0.19	1.60	15.35	13.19	0.53	1.33	41.03	14.00	11.85	0.15	0.76	0.00	0.00	0.00	0.03
5233-6	0.00	0.00	1.37	15.02	13.03	0.53	1.57	42.48	12.42	12.59	0.30	0.68	0.00	0.00	0.00	0.02
5233-6	0.00	0.00	1.32	13.77	12.79	0.41	1.26	42.40	14.19	12.80	0.27	0.80	0.00	0.00	0.00	0.00
5233-6	0.00	0.00	1.37	14.16	12.64	0.30	1.39	43.59	13.27	12.30	0.29	0.60	0.02	0.01	0.00	0.03
5233-6	0.00	0.00	2.05	18.99	14.48	0.41	1.22	37.18	13.57	11.46	0.14	0.47	0.03	0.00	0.00	0.00
5233-6	0.00	0.00	0.75	8.54	12.62	0.43	1.37	46.23	18.76	10.22	0.39	0.66	0.00	0.00	0.00	0.04
5233-6	0.00	0.00	0.18	2.53	9.04	0.19	1.53	52.87	17.70	14.68	0.33	0.92	0.00	0.02	0.01	0.00
5233-6	0.00	0.00	0.15	2.93	10.02	0.26	1.28	49.86	21.85	12.61	0.28	0.78	0.00	0.00	0.00	0.00
5233-6	0.00	0.00	1.95	17.52	13.40	0.55	1.54	40.26	12.87	10.98	0.25	0.66	0.02	0.00	0.00	0.00
5233-6	0.00	0.00	0.00	0.13	7.85	0.19	1.46	54.44	19.60	15.01	0.31	0.91	0.05	0.07	0.00	0.00
5233-6	0.00	0.00	1.25	12.71	12.78	0.53	1.06	42.38	15.85	12.75	0.20	0.39	0.04	0.04	0.00	0.00
5233-6	0.00	0.00	1.61	16.02	13.44	0.49	1.43	40.44	13.83	11.73	0.32	0.70	0.00	0.00	0.00	0.00
5233-6	0.00	0.28	0.48	5.65	10.20	0.32	1.61	50.49	16.71	13.30	0.19	0.76	0.00	0.00	0.00	0.00
5233-6	0.00	0.13	1.55	15.42	13.48	0.41	1.40	40.74	13.95	11.79	0.29	0.79	0.02	0.03	0.00	0.00
5233-6	0.00	0.00	1.06	10.96	12.39	0.53	1.54	42.30	16.35	13.76	0.30	0.77	0.02	0.03	0.00	0.00
5233-6	0.00	0.00	1.59	15.50	13.40	0.44	1.31	39.72	15.62	11.50	0.19	0.67	0.00	0.06	0.00	0.00
5233-6	0.00	0.00	2.62	21.42	14.67	0.42	1.32	35.45	12.71	10.61	0.17	0.57	0.03	0.02	0.00	0.00
5233-6	0.00	0.00	1.46	14.23	12.72	0.44	1.31	42.86	13.86	12.19	0.25	0.58	0.10	0.00	0.00	0.00
5233-6	0.99	0.00	2.47	20.66	14.57	0.47	1.25	34.24	13.72	10.78	0.15	0.56	0.08	0.03	0.01	0.00
5233-6	0.00	0.36	0.00	0.22	7.73	0.18	1.35	53.50	20.65	15.16	0.16	0.71	0.00	0.00	0.00	0.00
5233-6	0.22	1.00	0.40	5.08	9.95	0.25	1.26	50.05	16.93	13.69	0.21	0.87	0.02	0.00	0.03	0.05
5233-6	0.00	0.00	2.73	20.62	14.73	0.52	1.50	35.20	14.55	9.33	0.22	0.55	0.00	0.05	0.00	0.00
5233-6	0.53	0.32	1.60	14.10	12.18	0.51	1.39	43.88	12.56	12.27	0.30	0.34	0.03	0.00	0.00	0.00
5233-6	2.04	0.21	0.07	0.53	8.51	0.13	0.82	48.89	22.20	15.42	0.39	0.52	0.06	0.05	0.11	0.06
5233-6	0.29	0.45	1.66	15.50	12.49	0.33	0.27	44.04	12.90	11.39	0.07	0.52	0.04	0.02	0.02	0.03

Figure 9B

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-10	0.00	0.00	0.23	36.72	21.59	0.17	1.66	20.65	16.21	1.38	0.65	0.46	0.02	0.25	0.01	0.01
3863-10	0.00	0.00	0.33	42.87	18.70	0.30	1.72	18.86	14.79	1.36	0.57	0.40	0.02	0.05	0.01	0.01
3863-10	0.00	0.00	0.24	36.56	19.03	0.29	1.76	22.75	16.47	1.74	0.58	0.39	0.02	0.15	0.01	0.01
3863-10	0.00	0.00	0.32	42.65	19.06	0.33	2.26	18.58	14.01	1.43	0.68	0.33	0.03	0.27	0.02	0.03
3863-10	0.00	0.00	0.33	42.48	19.74	0.40	2.34	18.72	13.55	1.38	0.66	0.27	0.05	0.06	0.01	0.02
3863-10	0.00	0.00	0.33	42.88	18.88	0.30	1.95	17.73	15.44	1.44	0.64	0.27	0.04	0.08	0.02	0.01
3863-10	0.00	0.00	0.22	40.89	20.63	0.24	1.81	17.77	15.76	1.39	0.65	0.35	0.06	0.22	0.01	0.01
3863-10	0.00	0.00	0.20	29.49	17.06	0.24	1.86	28.63	19.46	1.68	0.58	0.66	0.05	0.06	0.01	0.02
3863-10	0.00	0.00	0.39	41.52	18.34	0.32	2.15	19.57	15.19	1.54	0.56	0.31	0.03	0.07	0.00	0.02
3863-10	0.00	0.00	0.30	37.55	20.00	0.23	1.79	23.58	13.87	1.47	0.59	0.51	0.03	0.05	0.02	0.02
3863-10	0.00	0.00	0.13	21.84	17.17	0.25	2.50	37.17	17.07	1.80	0.75	0.80	0.12	0.38	0.02	0.02
3863-10	0.00	0.00	0.14	25.13	17.66	0.23	2.00	31.52	20.07	1.42	0.65	0.81	0.05	0.29	0.01	0.00
3863-7	0.00	0.00	0.18	21.00	15.58	0.42	2.80	37.13	18.53	2.66	0.87	0.47	0.07	0.23	0.04	0.02
3863-7	0.00	0.00	0.14	16.64	14.67	0.38	2.99	38.90	21.75	2.91	0.81	0.56	0.08	0.13	0.03	0.02
3863-7	0.00	0.00	0.12	18.54	15.25	0.37	3.11	39.03	19.32	2.58	0.88	0.58	0.05	0.12	0.04	0.02
3863-7	0.00	0.00	0.12	18.55	14.81	0.38	3.16	37.62	20.65	3.20	0.82	0.42	0.02	0.19	0.03	0.02
3863-7	0.00	0.00	0.02	0.16	6.07	0.35	3.12	63.30	22.03	2.68	0.96	1.06	0.03	0.15	0.02	0.05
3863-7	0.00	0.00	0.14	16.90	14.90	0.41	2.97	40.23	20.11	2.83	0.79	0.63	0.05	0.02	0.01	0.02
3863-7	0.00	0.00	0.15	12.57	13.66	0.57	3.48	44.45	20.42	3.07	0.98	0.48	0.02	0.10	0.03	0.02
3863-7	0.00	0.00	0.11	10.22	12.64	0.58	3.83	46.53	20.86	3.35	1.14	0.46	0.03	0.19	0.03	0.04
3863-7	0.00	0.00	0.09	15.48	14.28	0.83	3.00	39.64	21.56	3.77	0.76	0.39	0.04	0.04	0.05	0.05
3863-7	0.00	0.00	0.08	10.89	12.79	0.54	3.00	46.69	21.23	3.54	0.76	0.29	0.04	0.03	0.09	0.03
3863-7	0.00	0.00	0.14	9.77	12.73	0.51	3.74	46.96	20.90	3.37	1.02	0.50	0.04	0.26	0.04	0.01
3863-7	0.00	0.00	0.16	15.86	14.25	0.51	3.46	41.12	19.50	3.32	0.89	0.60	0.07	0.17	0.03	0.04
3863-4	0.00	0.00	0.17	15.69	14.91	1.21	2.32	31.36	29.72	3.01	0.85	0.49	0.05	0.14	0.05	0.02
3863-4	0.00	0.00	0.23	38.63	19.96	0.29	1.41	20.94	15.70	1.39	0.62	0.54	0.03	0.25	0.01	0.01
3863-4	0.00	0.00	0.00	25.75	33.27	0.11	8.98	7.98	3.42	0.06	2.33	17.44	0.08	0.18	0.13	0.27
3863-4	0.00	0.00	0.17	30.59	19.06	0.26	1.70	27.57	17.30	1.41	0.76	0.74	0.04	0.38	0.01	0.01
3863-4	0.00	0.00	0.16	28.93	17.51	0.27	2.25	28.14	19.06	1.87	0.78	0.59	0.04	0.39	0.01	0.01
3863-4	0.00	0.00	0.19	31.48	18.44	0.21	2.06	28.98	15.77	1.37	0.71	0.65	0.03	0.09	0.01	0.01
3863-4	0.00	0.00	0.18	38.07	21.62	0.22	1.55	22.37	13.14	1.11	0.79	0.52	0.03	0.39	0.01	0.00

FIGURE 10A

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-4	0.00	0.00	0.18	29.22	18.35	0.34	2.02	29.70	16.70	1.58	0.74	0.79	0.06	0.29	0.01	0.01
3863-4	0.00	0.00	0.23	34.61	19.74	0.17	1.70	24.07	16.55	1.21	0.70	0.65	0.04	0.31	0.01	0.01
3863-4	0.00	0.00	0.18	30.56	18.47	0.19	2.08	28.61	16.81	1.50	0.68	0.63	0.04	0.24	0.01	0.01
3863-4	0.00	0.00	0.21	37.45	21.35	0.19	1.61	23.60	12.97	1.07	0.71	0.54	0.03	0.25	0.01	0.01
3863-4	0.00	0.00	0.18	29.70	18.98	0.19	2.03	29.00	16.70	1.36	0.77	0.73	0.00	0.36	0.01	0.01
3863-4	0.00	0.00	0.22	37.87	20.27	0.23	1.93	22.06	14.51	1.31	0.77	0.48	0.02	0.31	0.01	0.01
3863-4	0.00	0.00	0.21	39.14	21.36	0.19	1.64	21.46	13.42	1.13	0.69	0.37	0.09	0.30	0.01	0.00
3863-4	0.00	0.00	0.20	38.94	20.69	0.25	1.38	18.57	17.11	1.37	0.67	0.39	0.04	0.36	0.01	0.01
3863-4	0.00	0.00	0.01	0.21	5.81	0.32	4.29	65.31	18.68	2.19	1.38	1.19	0.01	0.59	0.01	0.01
3863-4	0.00	0.00	0.07	0.17	8.14	0.61	4.97	54.61	25.74	3.28	1.50	0.67	0.05	0.14	0.04	0.02
3863-4	0.00	0.00	0.16	30.31	19.06	0.26	1.92	27.23	17.65	1.58	0.76	0.72	0.03	0.32	0.00	0.01
3863-4	0.00	0.00	0.20	32.77	18.77	0.23	1.92	27.37	15.76	1.35	0.66	0.67	0.02	0.26	0.01	0.01
3863-4	0.00	0.00	0.28	37.97	19.58	0.34	1.74	21.75	15.46	1.60	0.66	0.46	0.03	0.10	0.01	0.01
3863-4	0.00	0.00	0.25	39.54	19.76	0.26	1.79	19.97	15.78	1.50	0.63	0.39	0.01	0.10	0.00	0.01
3863-4	0.00	0.00	0.19	31.46	18.50	0.17	2.00	30.06	14.81	1.30	0.75	0.66	0.01	0.07	0.01	0.01
3863-4	0.00	0.00	0.23	34.79	19.64	0.38	1.96	22.66	17.04	1.78	0.85	0.49	0.03	0.10	0.02	0.01
3863-4	0.00	0.00	0.21	31.55	18.70	0.23	2.16	27.97	15.73	1.44	0.83	0.70	0.04	0.40	0.01	0.01
3863-4	0.00	0.00	0.18	29.27	18.66	0.25	2.22	31.60	14.42	1.74	0.79	0.76	0.04	0.08	0.01	0.00
3863-4	0.00	0.00	0.58	50.92	32.69	0.46	4.72	5.73	2.75	0.16	1.17	0.39	0.06	0.28	0.05	0.05
3863-4	0.00	0.00	0.28	40.26	19.58	0.20	1.48	20.62	15.20	1.24	0.58	0.48	0.04	0.05	0.01	0.00
3863-4	0.00	0.00	0.20	32.09	18.27	0.17	2.03	28.26	15.99	1.43	0.71	0.74	0.04	0.05	0.01	0.01
3863-4	0.00	0.00	0.04	0.38	4.65	0.26	3.07	62.89	24.59	1.83	0.85	1.12	0.01	0.26	0.04	0.01
3863-4	0.00	0.00	0.19	30.34	18.77	0.28	1.83	25.81	19.41	1.46	0.73	0.77	0.03	0.36	0.01	0.02
3863-4	0.00	0.00	0.03	0.38	5.07	0.29	3.36	64.47	22.34	1.91	0.95	1.09	0.05	0.04	0.00	0.01
3863-4	0.00	0.00	0.22	37.53	20.33	0.30	1.87	21.73	15.14	1.30	0.80	0.46	0.03	0.29	0.01	0.01
3863-4	0.00	0.00	0.00	0.38	5.09	0.31	3.37	66.30	20.02	1.78	1.03	1.17	0.02	0.52	0.01	0.01
3863-4	0.00	0.00	0.02	0.38	4.79	0.23	3.87	68.32	17.76	1.98	1.07	1.16	0.01	0.37	0.02	0.01
3863-4	0.00	0.00	0.17	25.22	18.00	0.35	2.59	34.34	15.42	1.65	0.99	0.74	0.02	0.47	0.02	0.02
3863-4	0.00	0.00	0.17	29.76	18.99	0.21	2.32	31.59	13.69	1.20	0.86	0.78	0.04	0.38	0.01	0.01
3863-4	0.00	0.00	0.03	0.43	4.99	0.28	3.24	64.01	22.34	2.08	0.98	1.16	0.03	0.41	0.01	0.01
3863-8	0.00	0.00	0.02	0.10	5.32	0.31	3.67	61.45	24.35	2.55	0.96	1.14	0.02	0.09	0.01	0.02

FIGURE 10B

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-8	0.00	0.00	0.03	0.10	5.94	0.38	3.09	56.78	28.77	2.79	0.89	0.99	0.04	0.15	0.03	0.01
3863-8	0.00	0.00	0.04	0.14	5.78	0.36	3.44	64.06	21.60	2.45	0.91	1.02	0.02	0.15	0.02	0.02
3863-8	0.00	0.00	0.04	0.09	5.37	0.33	3.45	63.65	22.77	2.20	0.90	0.99	0.04	0.15	0.01	0.01
3863-8	0.00	0.00	0.08	0.09	6.57	0.45	4.04	58.85	24.60	3.22	1.00	0.84	0.04	0.19	0.02	0.02
3863-8	0.00	0.00	0.03	0.07	5.61	0.32	3.45	60.39	25.33	2.63	1.02	1.02	0.04	0.07	0.02	0.02
3863-8	0.00	0.00	0.02	0.12	5.80	0.42	3.87	66.16	18.67	2.47	1.03	0.89	0.10	0.40	0.01	0.02
3863-8	0.00	0.00	0.03	0.09	5.52	0.33	3.26	61.36	24.50	2.43	0.93	1.07	0.03	0.45	0.01	0.01
3863-8	0.00	0.00	0.02	0.15	5.25	0.25	3.14	62.11	24.32	2.41	0.85	1.08	0.04	0.36	0.01	0.01
3863-8	0.00	0.00	0.04	0.19	6.47	0.43	4.15	56.05	27.43	2.97	1.12	0.84	0.02	0.25	0.02	0.01
3863-8	0.00	0.00	0.03	0.16	6.13	0.38	3.48	59.94	24.95	2.68	0.97	0.86	0.05	0.33	0.02	0.01
3863-8	0.00	0.00	0.03	0.09	5.65	0.36	3.71	61.34	24.00	2.58	0.98	1.00	0.08	0.18	0.01	0.01
3863-2	0.00	0.00	0.22	26.95	17.05	0.28	2.31	32.94	15.90	2.37	0.84	0.64	0.11	0.36	0.02	0.01
3863-2	0.00	0.00	0.09	0.81	8.05	0.74	3.06	58.33	22.87	3.86	0.94	0.82	0.04	0.29	0.06	0.03
3863-2	0.00	0.00	0.13	19.27	15.52	0.42	2.89	40.66	16.82	2.47	0.91	0.68	0.02	0.17	0.02	0.01
3863-2	0.00	0.00	0.15	24.15	17.73	0.32	2.18	36.80	14.75	1.69	0.85	0.84	0.04	0.47	0.01	0.01
3863-2	0.00	0.00	0.19	25.37	17.25	0.25	2.66	32.97	17.44	1.67	0.94	0.78	0.01	0.45	0.00	0.01
3863-2	0.00	0.00	0.04	0.59	7.21	0.67	2.91	56.35	26.68	2.99	1.06	0.92	0.07	0.44	0.02	0.05
3863-2	0.00	0.00	0.20	27.82	18.08	0.37	2.56	33.69	13.30	1.77	0.97	0.68	0.02	0.51	0.01	0.03
3863-2	0.00	0.00	0.13	20.71	17.03	0.29	2.72	37.93	16.70	1.84	1.13	0.80	0.01	0.68	0.01	0.01
3863-2	0.00	0.00	0.17	26.25	17.87	0.22	2.26	37.01	12.61	1.48	0.85	0.82	0.05	0.41	0.01	0.00
3863-2	0.00	0.00	0.14	22.96	16.51	0.28	2.58	38.26	15.70	1.91	0.80	0.76	0.03	0.06	0.02	0.01
3863-2	0.00	0.00	0.15	22.04	16.77	0.20	2.61	40.01	14.57	1.96	0.81	0.71	0.04	0.11	0.02	0.01
3863-2	0.00	0.00	0.02	0.28	5.70	0.34	3.24	65.13	20.60	2.42	1.08	1.03	0.01	0.08	0.03	0.02
3863-5	0.00	0.00	0.17	23.40	16.42	0.41	2.44	32.08	21.06	2.40	0.80	0.61	0.02	0.14	0.02	0.02
3863-5	0.00	0.00	0.25	27.71	15.98	0.45	2.68	28.97	20.24	2.49	0.60	0.46	0.03	0.10	0.03	0.03
3863-5	0.00	0.00	0.20	28.26	17.16	0.32	2.23	31.84	16.72	1.68	0.74	0.68	0.03	0.13	0.01	0.01
3863-5	0.00	0.00	0.16	19.06	15.20	0.51	3.02	36.54	21.29	2.76	0.92	0.38	0.02	0.10	0.01	0.01
3863-5	0.00	0.00	0.03	0.29	6.06	0.37	3.26	53.48	31.80	2.74	0.78	0.88	0.05	0.18	0.04	0.03
3863-5	0.00	0.00	0.26	25.74	16.20	0.51	2.92	31.55	18.82	2.53	0.86	0.46	0.03	0.09	0.02	0.01
3863-5	0.00	0.00	0.19	20.65	15.48	0.38	2.76	35.90	20.56	2.54	0.78	0.61	0.06	0.06	0.01	0.02
3863-5	0.00	0.00	0.19	25.88	16.67	0.31	2.38	34.81	16.50	1.90	0.72	0.54	0.04	0.03	0.02	0.02

FIGURE 10C

SAMPLE	%8:0	%10:0	%12:0	%14:0	%16:0	%16:1	%18:0	%18:1	%18:2	%18:3	%20:0	%20:1	%20:2	%22:0	%22:1	%22:2
3863-5	0.00	0.00	0.20	29.58	16.88	0.31	2.01	28.68	18.97	1.82	0.62	0.69	0.03	0.17	0.01	0.02
3863-5	0.00	0.00	0.07	0.76	8.04	0.69	4.85	52.50	26.95	3.82	1.21	0.84	0.02	0.19	0.04	0.03
3863-5	0.00	0.00	0.14	16.17	14.15	0.57	3.81	37.23	23.14	3.08	0.98	0.53	0.03	0.09	0.02	0.04
3863-5	0.00	0.00	0.30	38.75	18.50	0.27	1.71	21.34	16.39	1.57	0.64	0.44	0.03	0.04	0.02	0.01

FIGURE 10D

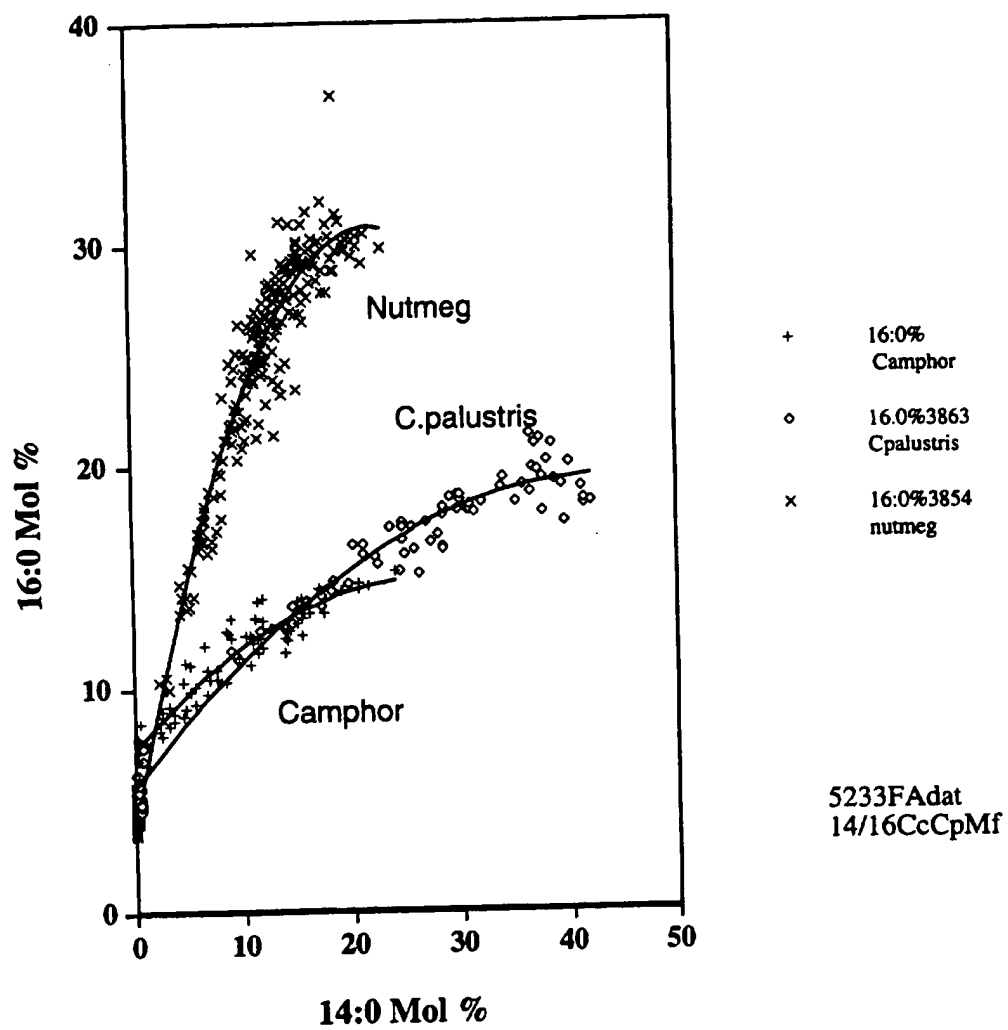


FIGURE 11

STRAIN_ID	8:0	10:0	12:0	14:0	16:0	16:1	18:0	18:1	18:2	18:3	20:0	20:1	20:2	22:0	22:1	22:2	24:0	24:1
3857-1	0	0.17	0.03	0.10	4.92	0.27	2.94	67.48	20.39	1.42	0.80	1.07	0.06	0.35	0	0	0	0
3857-2	0	0.16	0.25	10.94	23.01	0.73	5.74	37.57	17.82	1.19	1.48	0.59	0.02	0.49	0	0	0	0
3857-3	0	0.18	0.20	8.20	19.90	0.60	6.02	43.84	17.02	1.32	1.49	0.67	0.03	0.51	0	0	0	0
3857-4	0	0.18	0.23	11.15	28.00	0.94	5.44	30.86	19.46	1.44	1.37	0.47	0.00	0.46	0	0	0	0
3857-5	0	0.15	0.12	5.47	17.47	0.57	4.72	46.31	21.17	1.52	1.27	0.76	0.00	0.46	0	0	0	0
3857-7	0	0.16	0.14	5.00	14.03	0.53	4.29	52.91	19.24	1.39	1.11	0.79	0.01	0.40	0.01	0	0	0
3857-8	0	0.17	0.21	9.48	21.90	0.75	5.43	39.22	19.12	1.30	1.33	0.60	0.03	0.45	0	0	0	0
3857-9	0	0.15	0.19	8.65	20.70	0.63	5.57	42.80	17.57	1.27	1.37	0.64	0.01	0.45	0	0	0	0
3857-10	0	0.14	0.25	10.92	26.41	0.78	6.70	34.63	16.16	1.27	1.67	0.47	0.03	0.57	0.01	0	0	0
3857-11	0	0.16	0.14	5.75	17.17	0.63	5.04	46.43	20.68	1.46	1.31	0.70	0.04	0.49	0	0	0	0
3857-12	0	0.18	0.13	4.38	15.86	0.75	4.96	47.97	21.66	1.55	1.25	0.75	0.01	0.53	0.01	0	0	0
3857-13	0	0.17	0.18	7.18	18.93	0.67	5.29	43.03	20.70	1.40	1.28	0.67	0.04	0.45	0	0	0	0
3857-14	0	0.25	0.17	5.81	17.94	0.79	4.96	40.28	25.58	1.75	1.25	0.67	0.05	0.51	0	0	0	0
3857-15	0	0.20	0.13	4.52	14.83	0.63	4.21	47.22	24.45	1.58	1.03	0.74	0.05	0.39	0	0	0	0
3857-16	0	0.18	0.21	9.47	21.28	0.62	5.65	39.68	19.07	1.29	1.39	0.64	0.01	0.49	0	0	0	0
3857-17	0	0.17	0.13	5.62	17.52	0.60	4.88	47.62	19.75	1.35	1.19	0.71	0.04	0.43	0	0	0	0
3857-18	0	0.21	0.05	0.12	5.20	0.31	2.82	63.74	23.92	1.63	0.69	0.96	0.06	0.30	0	0	0	0
3857-19	0	0.18	0.17	6.95	19.06	0.69	5.24	43.48	20.57	1.37	1.22	0.65	0.01	0.42	0	0	0	0
3857-20	0	0.21	0.15	5.91	16.71	0.54	5.43	47.68	19.32	1.42	1.34	0.75	0.04	0.50	0	0	0	0
3864-2	0	0.19	0.28	23.17	20.08	0.33	2.08	27.83	22.17	1.69	0.67	0.80	0.08	0.33	0.28	0	0	0
3864-3	0	0.14	0.14	16.71	13.55	0.23	2.33	46.35	17.62	1.17	0.64	0.83	0.03	0.26	0	0	0	0
3864-4	0	0.19	0.08	3.12	6.89	0.31	2.67	61.32	22.05	1.47	0.65	0.91	0.06	0.28	0	0	0	0
3864-5	0	0.15	0.12	15.38	13.36	0.26	2.11	45.23	20.23	1.33	0.61	0.87	0.06	0.27	0.01	0	0	0
3864-6	0	0.12	0.14	17.86	14.65	0.30	1.90	38.82	23.07	1.48	0.56	0.78	0.07	0.25	0	0	0	0
3864-7	0	0.16	0.17	16.15	15.07	0.28	2.15	43.01	19.71	1.43	0.66	0.82	0.07	0.32	0	0	0	0
3864-8	0	0.14	0.20	22.94	18.12	0.24	2.04	34.27	19.13	1.23	0.62	0.74	0.06	0.26	0	0	0	0
3864-9	0	0.15	0.31	34.82	21.52	0.29	2.02	17.67	19.80	1.65	0.77	0.47	0.07	0.40	0.06	0	0	0
3864-10	0	0.11	0.16	21.21	15.67	0.25	1.72	35.98	22.00	1.32	0.53	0.75	0.06	0.24	0	0	0	0
3864-11	0	0.11	0.11	14.65	13.34	0.27	2.00	43.48	22.98	1.32	0.58	0.83	0.06	0.26	0	0	0	0
3864-16	0	0.13	0.14	17.73	14.18	0.26	1.98	40.29	22.37	1.35	0.55	0.76	0.01	0.24	0	0	0	0

FIGURE 12

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 96/01585

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/82 C12N15/55 A01H5/00 C11B1/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N A01H C11B

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO,A,94 10288 (CALGENE INC ;VOELKER TONI ALOIS (US); DAVIES HUW MAELOR (US); KNUT) 11 May 1994	1-3,8, 21,22
Y	see page 24, line 29 - page 25, line 5 see page 32 - page 34 see page 32, line 32 - page 34, line 25 see figure 8 see figure 1 ---	4-6
X	WO,A,92 20236 (CALGENE INC) 26 November 1992	21
Y	see page 5, line 16 - line 28 see page 38, line 35 - page 40 see page 44, line 24 - page 50A see page 64, line 22 - line 29 see figure 5B; example 5 see figure 1A --- -/--	4-6



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents:

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Date of the actual completion of the international search

25 September 1996

Date of mailing of the international search report

18.10.96

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Maddox, A

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 96/01585

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
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O,X	KADER, J.-C. AND P. MAZLIAK (ED.). PLANT LIPID METABOLISM; 11TH INTERNATIONAL MEETING ON PLANT LIPIDS, PARIS, FRANCE, JUNE 26-JULY 1, 1994. XX+588P. KLUWER ACADEMIC PUBLISHERS: DORDRECHT, NETHERLANDS; NORWELL, MASSACHUSETTS, USA. 0 (0). 1995. 495-498., XP000600383 MARTINI N., ET AL: "Expression of acyl-(ACP) thioesterase in Cuphea lanceolata and in transgenic rapeseed." see the whole document ---	22
P,X	SCIENCE (WASHINGTON D C) 268 (5211). 1995. 681-686. , XP002014017 TOEPFER R., ET AL: "Modification of plant lipid synthesis." see page 684, right-hand column; figure 3 ---	1-6,8,9, 12,14, 15,18-22
P,X	WO,A,95 06740 (MAX PLANCK GESELLSCHAFT ;TOEPFER REINHARD (DE); MARTINI NORBERT (D) 9 March 1995 see page 13, last paragraph - page 16 ---	1-6,9, 12,14, 15,18-22
P,X	WO,A,95 13390 (CALGENE INC ;VOELKER TONI ALOIS (US); YUAN LING (US); KRIDL JEAN () 18 May 1995 see page 51; figures 5A-E see figures 9A-F see figure 14 ---	15,18-21
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INTERNATIONAL SEARCH REPORT

International Application No
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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
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